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US-09-925-637-63.rn1

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GenCore version 5.1.6  
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CM nucleic - nucleic search, using sw model

Run on: April 20, 2004, 07:00:11 ; Search time 94 Seconds  
(without alignments)  
5083.114 Million cell updates/sec

Title: US-09-925-637-63

Perfect score: 861 atgacgaatcaccgatgaa.....tattagaatcgttattta 861

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ins/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ins/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ins/5A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ins/5B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ins/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ins/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	861	100.0	1893	4 US-08-956-171E-155	Sequence 155, App
2	606	70.4	882	4 US-09-276-873-1	Sequence 1, Appl
3	25	2.9	909	4 US-09-134-001C-134	Sequence 334, App
C 4	19	2.2	640681	4 US-09-790-988-1	Sequence 1, Appl
5	18	2.1	753	4 US-09-484-970B-110	Sequence 110, App
6	18	2.1	1301	1 US-07-686-322A-1	Sequence 1, Appl
7	18	2.1	1301	1 US-08-002-899-1	Sequence 1, Appl
8	18	2.1	5163	3 US-08-700-651-1	Sequence 1, Appl
9	18	2.1	5163	3 US-08-928-951B-4	Sequence 4, Appl
10	18	2.1	5163	4 US-09-588-995A-4	Sequence 4, Appl
11	18	2.1	5318	3 US-08-700-651-2	Sequence 2, Appl
12	18	2.1	5318	3 US-08-928-951B-3	Sequence 3, Appl
13	18	2.1	5318	3 US-08-956-171E-243	Sequence 243, App
14	18	2.1	10146	4 US-08-956-171E-243	Sequence 243, App
15	18	2.1	786431	4 US-09-751-589-3	Sequence 3, Appl
C 16	18	2.1	786431	4 US-09-751-589-3	Sequence 3, Appl
17	17	2.0	540	4 US-09-702-705-1416	Sequence 1416, Ap
18	17	2.0	540	4 US-09-736-457-1416	Sequence 1416, Ap
19	17	2.0	540	4 US-09-614-124B-1416	Sequence 1416, Ap
20	17	2.0	540	4 US-09-671-325-1416	Sequence 1416, Ap
21	17	2.0	604	3 US-09-385-982-404	Sequence 404, App
22	17	2.0	616	3 US-09-385-982-173	Sequence 173, App
23	17	2.0	660	2 US-08-902-516-1	Sequence 1, Appl
24	17	2.0	660	4 US-09-847-185-1	Sequence 1, Appl
25	17	2.0	1132	4 US-09-203-958A-1	Sequence 1, Appl
26	17	2.0	1135	4 US-09-203-958A-3	Sequence 3, Appl
27	17	2.0	1164	4 US-09-134-001C-2199	Sequence 2199, Ap

28	17	2.0	1239	4 US-09-543-681A-4146	Sequence 4146, Ap
29	17	2.0	1511	2 US-08-809-763-3	Sequence 3, Appl
30	17	2.0	1511	3 US-08-956-253-3	Sequence 3, Appl
31	17	2.0	2335	2 US-08-300-584-3	Sequence 3, Appl
32	17	2.0	2335	2 US-08-476-123-3	Sequence 3, Appl
33	17	2.0	2517	4 US-09-328-352-3410	Sequence 3410, Ap
C 34	17	2.0	2517	4 US-09-371-338-20	Sequence 20, Appl
35	17	2.0	3374	4 US-09-205-258-184	Sequence 184, App
C 36	17	2.0	4656	3 US-09-150-460B-4	Sequence 4, Appl
C 37	17	2.0	6085	4 US-09-800-729-35	Sequence 35, Appl
C 38	17	2.0	6614	3 US-09-150-460B-3	Sequence 3, Appl
39	17	2.0	7258	4 US-09-058-483-8	Sequence 8, Appl
40	17	2.0	14561	4 US-09-392-714-1	Sequence 1, Appl
C 41	17	2.0	193303	4 US-09-497-855A-37	Sequence 37, Appl
C 42	17	2.0	193303	4 US-09-497-855A-44	Sequence 44, Appl
C 43	17	2.0	580073	4 US-08-545-528D-1	Sequence 1, Appl
C 44	17	2.0	1664976	4 US-08-916-421B-1	Sequence 1, Appl
C 45	17	2.0	4403765	3 US-09-103-640A-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-08-956-171E-155/c  
Sequence 155, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 155:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1893 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 155:  
US-08-956-171E-155

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Query Match 100.0%; Score 861; DB 4; Length 1893;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCGAATCTACCGATGATTAATTAATGATGAAGTCAATTAATGATTAATCGGTGGC 60
DB 1314 ATGCGAATCTACCGATGATTAATTAATGATGAAGTCAATTAATGATTAATCGGTGGC 1255
QY 61 ATAAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
DB 1254 ATAAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1195
QY 121 GGAGGTAAAGCAGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 180
DB 1194 GGAGGTAAAGCAGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 1135
QY 181 TATGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 1134 TATGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1075
QY 241 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 1074 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1015
QY 301 AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 1014 AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 955
QY 361 GAATCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 954 GAATCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 895
QY 421 CTGTCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 894 CTGTCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 835
QY 481 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 834 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 775
QY 541 TTATTAATCTTTGGGTTATGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 774 TTATTAATCTTTGGGTTATGATGATGATGATGATGATGATGATGATGATGATGATG 715
QY 601 GAACATTTAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 714 GAACATTTAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 655
QY 661 TTGACCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 654 TTGACCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 595
QY 721 AATAAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
DB 594 AATAAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 535
QY 781 CATAGAGCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 534 CATAGAGCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 475
QY 841 TTATTAAGAAATCGTTGATTTA 861
DB 474 TTATTAAGAAATCGTTGATTTA 454
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RESULT 2  
US-09-276-873-1  
Sequence 1, Application US/09276873  
Patent No. 6107058  
GENERAL INFORMATION:  
APPLICANT: Wilding, Edwin Imogen  
APPLICANT: Gwynn, Michael  
TITLE OF INVENTION: Ispa

FILE REFERENCE: GMI0208  
CURRENT APPLICATION NUMBER: US/09/276, 873  
CURRENT FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 882  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-09-276-873-1

Query Match 70.4%; Score 606; DB 3; Length 882;  
Best Local Similarity 99.4%; Pred. No. 76-297;  
Matches 856; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ATGCGAATCTACCGATGATTAATTAATGATGAAGTCAATTAATGATTAATCGGTGGC 60
DB 1 ATGCGAATCTACCGATGATTAATTAATGATGAAGTCAATTAATGATTAATCGGTGGC 60
QY 61 ATAAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
DB 61 ATAAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 121 GGAGGTAAAGCAGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 180
DB 121 GGAGGTAAAGCAGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 180
QY 181 TATGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 181 TATGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 241 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 241 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 301 AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 301 AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 361 GAATCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 GAATCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 CTGTCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 421 CTGTCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 481 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 541 TTATTAATCTTTGGGTTATGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 541 TTATTAATCTTTGGGTTATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 601 GAACATTTAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 GAACATTTAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 TTGACCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 TTGACCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 AATAAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
DB 721 AATAAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 CATAGAGCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 781 CATAGAGCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 TTATTAAGAAATCGTTGATTTA 861
DB 841 TTATTAAGAAATCGTTGATTTA 861
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Db 841 TTATTAGAAATCGTTGATTTA 861

RESULT 3

US-09-134-001C-334  
 ; Sequence 334, Application US/09134001C  
 ; Patent No. 6380370  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
 ; FILE REFERENCE: GTC-007  
 ; CURRENT APPLICATION NUMBER: US/09/134,001C  
 ; PRIOR FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: US 60/064,964  
 ; PRIOR FILING DATE: 1997-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/055,779  
 ; PRIOR FILING DATE: 1997-08-14  
 ; NUMBER OF SEQ ID NOS: 5674  
 ; SEQ ID NO 334  
 ; LENGTH: 909  
 ; TYPE: DNA  
 ; ORGANISM: Staphylococcus epidermidis  
 US-09-134-001C-334

Query Match 2.9%; Score 25; DB 4; Length 909;  
 Best Local Similarity 100.0%; Pred. No. 0.0051;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 281 GAGGAAATTAACAATCATTAAGT 305  
 308 GAGGAAATTAACAATCATTAAGT 332

RESULT 4

US-09-790-988-1/c  
 ; Sequence 1, Application US/09790988  
 ; Patent No. 6632935  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHIGENOBU, SHUJI  
 ; APPLICANT: MATANABE, HIDEKI  
 ; APPLICANT: HATTORI, MASAHIRA  
 ; APPLICANT: SAKAKI, YOSHIYUKI  
 ; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
 ; FILE REFERENCE: 081356/0159  
 ; CURRENT APPLICATION NUMBER: US/09/790,988  
 ; PRIOR FILING DATE: 2001-02-23  
 ; PRIOR APPLICATION NUMBER: JP2000-107160  
 ; PRIOR FILING DATE: 2000-04-07  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 1  
 ; TYPE: DNA  
 ; ORGANISM: Buchnera sp.  
 US-09-790-988-1

Query Match 2.2%; Score 19; DB 4; Length 640681;  
 Best Local Similarity 100.0%; Pred. No. 6.9;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 AATAAATTATAGATGAAG 37  
 Db 214082 AATAAATTATAGATGAAG 214064

RESULT 5

US-09-484-970B-110  
 ; Sequence 110, Application US/09484970B  
 ; Patent No. 6426186  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jones, Karen A.  
 ; APPLICANT: Volkmuth, Wayne

APPLICANT: Walker, Michael G.  
 ; TITLE OF INVENTION: BONE REMODELING GENES  
 ; FILE REFERENCE: PB-0014 US  
 ; CURRENT APPLICATION NUMBER: US/09/484,970B  
 ; PRIOR FILING DATE: 2000-01-18  
 ; NUMBER OF SEQ ID NOS: 172  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 110  
 ; LENGTH: 763  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. 6426186 009051.5CB1  
 US-09-484-970B-110

Query Match 2.1%; Score 18; DB 4; Length 763;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GATGAAATTAATTAATGA 32  
 Db 212 GATGAAATTAATTAATGA 229

RESULT 6

US-07-686-322A-1  
 ; Sequence 1, Application US/07686322A  
 ; Patent No. 5312733  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MacLeod Dr., Carol L.  
 ; TITLE OF INVENTION: No. 5312733el T-cell lymphoma CDNA clones  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Patent Department, Fulbright & Jaworski  
 ; STREET: 1301 McKinney, Suit 5100  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77010-3095  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/686,322A  
 ; FILING DATE: 19910411  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/509684  
 ; FILING DATE: 13-APR-1990  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: launer, Charlene A.  
 ; REGISTRATION NUMBER: 33,035  
 ; REFERENCE/DOCKET NUMBER: D-5232-CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (713) 651-3634  
 ; TELEFAX: (713) 651-5246  
 ; TELEX: Western Union 762829  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1301 base pairs  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Mouse  
 ; STRAIN: AKR1 Jackson  
 ; INDIVIDUAL ISOLATE: SL12 cell line  
 ; TISSUE TYPE: lymphoma  
 ; CELL TYPE: T-cell

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CELL LINE: SL12.3 and SL12.4  
IMMEDIATE SOURCE:  
CLONE: 19.1  
US-07-686-322A-1

Query Match 2.1%; Score 18; DB 1; Length 1301;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 CCAATCAAAACCTTATT 845  
DB 3 CCAATCAAAACCTTATT 20

RESULT 7  
US-08-002-999-1  
Sequence 1, Application US/08002999  
Patent No. 5440017  
GENERAL INFORMATION:  
APPLICANT: Macleod Dr., Carol L.  
TITLE OF INVENTION: No. 5440017el T-cell lymphoma CDNA clones  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patent Department, Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/002,999  
FILING DATE: 19930111  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/686,322  
FILING DATE: 11-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Benjamin A.  
REGISTRATION NUMBER: 35,423  
REFERENCE/DOCKET NUMBER: D-5232-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 651-5587  
TELEFAX: (713) 651-5246  
TELEX: Western Union 762829  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1301 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: AKR1 Jackson  
INDIVIDUAL ISOLATE: SL12 cell line  
TISSUE TYPE: Lymphoma  
CELL LINE: T-cell  
CELL LINE: SL12.3 and SL12.4  
IMMEDIATE SOURCE:  
CLONE: 19.1  
US-08-002-999-1

Query Match 2.1%; Score 18; DB 1; Length 1301;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 CCAATCAAAACCTTATT 845  
DB 3 CCAATCAAAACCTTATT 20

DB 3 CCAATCAAAACCTTATT 20

RESULT 8  
US-08-700-651-1  
Sequence 1, Application US/08700651B  
Patent No. 6015882  
GENERAL INFORMATION:  
APPLICANT: PETERSEN, CAROLYN  
APPLICANT: LEECH, JAMES  
APPLICANT: NELSON, RICHARD, C.  
APPLICANT: GUY, JIRI  
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAs AND RNAs  
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum  
TITLE OF INVENTION: INFECTIONS  
FILE REFERENCE: 480.19-4(HV)  
CURRENT APPLICATION NUMBER: US/08/700,651B  
CURRENT FILING DATE: 1997-08-14  
EARLIER APPLICATION NUMBER: 08/415,751  
EARLIER FILING DATE: 1995-04-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 5163  
TYPE: DNA  
ORGANISM: Cryptosporidium parvum  
US-08-700-651-1

Query Match 2.1%; Score 18; DB 3; Length 5163;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATGATCTTGAAGT 507  
DB 3769 CCAATGATCTTGAAGT 3786

RESULT 9  
US-08-928-361B-4  
Sequence 4, Application US/08928361B  
Patent No. 6071518  
GENERAL INFORMATION:  
APPLICANT: Petersen, Carolyn  
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,  
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS  
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM  
TITLE OF INVENTION: SPECIES INFECTIONS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PETERSEN, VERNY, JONES & BIKSA  
STREET: 385 Sherman Avenue, Suite 6  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306-1840  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,361B  
FILING DATE: 12-SEP-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,062  
FILING DATE: 13-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: VERNY, HANA  
REGISTRATION NUMBER: 30,518  
REFERENCE/DOCKET NUMBER: 480.76-1(HV)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-1677



TELEFAX: 650-324-1678  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5163 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-928-361B-4

Query Match 2.1%; Score 18; DB 3; Length 5163;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAAGT 507  
DB 3769 CCAATTGATCTTGAAGT 3786

RESULT 10  
US-09-588-995A-4  
Sequence 4, Application US/09588995A  
Patent No. 6514697  
GENERAL INFORMATION:  
APPLICANT: PETERSEN, CAROLYN  
APPLICANT: BARNES, DEBRA A.  
APPLICANT: NELSON, RICHARD C.  
APPLICANT: GUT, JIRI  
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND  
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM  
TITLE OF INVENTION: INFECTIONS  
FILE REFERENCE: 480.19-5  
CURRENT APPLICATION NUMBER: US/09/588,995A  
CURRENT FILING DATE: 2000-06-06  
PRIOR APPLICATION NUMBER: 08/827,171  
PRIOR FILING DATE: 1997-03-27  
PRIOR APPLICATION NUMBER: 08/928,361  
PRIOR FILING DATE: 1997-09-12  
PRIOR APPLICATION NUMBER: 08/700,651  
PRIOR FILING DATE: 1996-08-14  
PRIOR APPLICATION NUMBER: 08/415,751  
PRIOR FILING DATE: 1995-04-03  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 5163  
TYPE: DNA  
ORGANISM: Cryptosporidium parvum  
US-09-588-995A-4

Query Match 2.1%; Score 18; DB 4; Length 5163;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAAGT 507  
DB 3769 CCAATTGATCTTGAAGT 3786

RESULT 11  
US-08-700-651-2  
Sequence 2, Application US/08700651B  
Patent No. 6015882  
GENERAL INFORMATION:  
APPLICANT: PETERSEN, CAROLYN  
APPLICANT: LEECH, JAMES  
APPLICANT: NELSON, RICHARD, C.  
APPLICANT: GUT, JIRI  
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAs AND RNAs  
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIDIUM PARVUM  
FILE REFERENCE: 480.19-4 (HV)  
CURRENT APPLICATION NUMBER: US/08/700,651B

CURRENT FILING DATE: 1997-08-14  
EARLIER APPLICATION NUMBER: 08/415,751  
EARLIER FILING DATE: 1995-04-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 5318  
TYPE: DNA  
ORGANISM: Cryptosporidium parvum  
US-08-700-651-2

Query Match 2.1%; Score 18; DB 3; Length 5318;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAAGT 507  
DB 3769 CCAATTGATCTTGAAGT 3786

RESULT 12  
US-08-928-361B-3  
Sequence 3, Application US/08928361B  
Patent No. 6071518  
GENERAL INFORMATION:  
APPLICANT: Petersen, Carolyn  
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,  
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS  
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM  
TITLE OF INVENTION: SPECIES INFECTIONS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSER: PETERS, VERNY, JONES & BIKSA  
STREET: 385 Sherman Avenue, Suite 6  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306-1840  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,361B  
FILING DATE: 12-SEP-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,062  
FILING DATE: 13-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: VERNY, HANA  
REGISTRATION NUMBER: 30,518  
REFERENCE/DOCKET NUMBER: 480.76-1 (HV)  
TELEPHONE: 650-324-1677  
TELEFAX: 650-324-1678  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5318 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-928-361B-3

Query Match 2.1%; Score 18; DB 3; Length 5318;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAAGT 507  
DB 3769 CCAATTGATCTTGAAGT 3786

Tue Apr 20 12:43:37 2004

US-09-925-637-63.inl

Page 6

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RESULT 13
US-09-588-995A-3
Sequence 3, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: NELSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3
LENGTH: 5318
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-09-588-995A-3

Query Match      2.1% Score 18; DB 4; Length 5318;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      490 CCAATTGATCTTGAACCT 507
DB      3769 CCAATTGATCTTGAACCT 3786

RESULT 14
US-08-956-171E-243
Sequence 243, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
```

```

FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
LENGTH: 10146 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 243:

US-08-956-171E-243

Query Match      2.1% Score 18; DB 4; Length 10146;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      319 ACTGCCATTTAGCAGCT 336
DB      9771 ACTGCCATTTAGCAGCT 9788

RESULT 15
US-09-751-389-3
Sequence 3, Application US/09751389
Patent No. 6630334
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: C1001067
CURRENT APPLICATION NUMBER: US/09/751,389
CURRENT FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 786431
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(786431)
OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Query Match      2.1% Score 18; DB 4; Length 786431;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      613 AGTTATGTTATCATTTA 630
DB      3108 AGTTATGTTATCATTTA 3125

Search completed: April 20, 2004, 08:09:37
Job time : 107 secs
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Tue Apr 20 12:43:37 2004

us-09-925-637-63.rnpb

Page 2

Db	61	ATPAAATPAAATCGATATGATATCTAGTGAAGAAAGATGTTGATATTCATTTAAATGCT	120
Qy	121	GGAGGTAACGCATCCGACCAAGTTCGTATTTACTCACTTATGATTCATTAATACGAG	180
Db	121	GGAGGTAACGCATCCGACCAAGTTCGTATTTACTCACTTATGATTCATTAATACGAG	180
Qy	181	TATGATTTAGTATGAAGAAGCCAAATTCGACTAAGAAATGATTCATATATTCATTTAT	240
Db	181	TATGATTTAGTATGAAGAAGCCAAATTCGACTAAGAAATGATTCATATATTCATTTAT	240
Qy	241	CATGATGACCTTACCAACGCGATGGATATATGATTTATGACAGAGAAATTTACAAATCAT	300
Db	241	CATGATGACCTTACCAACGCGATGGATATATGATTTATGACAGAGAAATTTACAAATCAT	300
Qy	301	AAAGTATATGCTGAGTGAATCTGCGATTTAGACGGTGAATGCTTTATTTACTAAAGCATTT	360
Db	301	AAAGTATATGCTGAGTGAATCTGCGATTTAGACGGTGAATGCTTTATTTACTAAAGCATTT	360
Qy	361	GAACTATTTTCAAGTATGATATGATTTAACTGATGATGAAGTAAATTAAGTTCTTACAAACG	420
Db	361	GAACTATTTTCAAGTATGATATGATTTAACTGATGATGAAGTAAATTAAGTTCTTACAAACG	420
Qy	421	CTGTCAATATGACAAGTGTGTCATGTTGGAATGCTCGCGGCTCAATGTTAGATATGCAAAAGC	480
Db	421	CTGTCAATATGACAAGTGTGTCATGTTGGAATGCTCGCGGCTCAATGTTAGATATGCAAAAGC	480
Qy	481	GAAAGCCAAACCAATTTGATCTTGTAAATCTTGAAATGATATACCAAAACAAAAACAGAGCA	540
Db	481	GAAAGCCAAACCAATTTGATCTTGTAAATCTTGAAATGATATACCAAAACAAAAACAGAGCA	540
Qy	541	TTATTAACCTTTTGCCTGTTATGAGTCCAGACAGATATCGTAAATGTCATGATACAACTTAA	600
Db	541	TTATTAACCTTTTGCCTGTTATGAGTCCAGACAGATATCGTAAATGTCATGATACAACTTAA	600
Qy	601	GAACTATTGAAAGTATATATGATATTAAGTATGATGTCACGATTTAAAGATGATTTA	660
Db	601	GAACTATTGAAAGTATATATGATATTAAGTATGATGTCACGATTTAAAGATGATTTA	660
Qy	661	TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	720
Db	661	TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	720
Qy	721	AATPAAAGTATCGTACGTGATTTATTTAGGAAAGATGCGCGAAGATTAATGACTTAT	780
Db	721	AATPAAAGTATCGTACGTGATTTATTTAGGAAAGATGCGCGAAGATTAATGACTTAT	780
Qy	781	CATGAGAGACGACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	840
Db	781	CATGAGAGACGACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	840
Qy	841	TTATTAGAAATCGTTGATTTA	861
Db	841	TTATTAGAAATCGTTGATTTA	861

RESULT 2  
 US-10-084-205-63  
 ; Sequence 63, Application US/10084205  
 ; Publication No. US20030049648A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Choi, Gil  
 ; TITLE OR INVENTION: 37 *Staphylococcus aureus* Genes and Polypeptides  
 ; FILE REFERENCE: PB515P1  
 ; CURRENT APPLICATION NUMBER: US/10/084,205  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23773  
 ; PRIOR FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: 60/151,933  
 ; PRIOR FILING DATE: 1999-09-01  
 ; NUMBER OF SEQ ID NOS: 74  
 ; SOFTWARE: PatentIn Ver. 3.1

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; LENGTH: 861
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-084-205-63

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Query Match	100.0%	Score 861;	DB 15;	Length 861;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 861;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGACGATCAACCGAAGAAATTAATTAATAGTAAGCAATTAATGAATTCGGTTCG	60
Db	1	ATGACGATCTACCGAGTAATTAATTAATAGTAAGCAATTAATGAATTCGGTTCG	60
QY	61	ATAATAAATCAGTAATGATTAAGTCTACGCTAGAGAAAGTAATGTTGATTCATTAATGCT	120
Db	61	ATAATAAATCAGTAATGATTAAGTCTACGCTAGAGAAAGTAATGTTGATTCATTAATGCT	120
QY	121	GGAGGTAAAGCCATCCGACAGTCTGTATTAATCACTTTAGATTCCTAAATACCGAG	180
Db	121	GGAGGTAAAGCCATCCGACAGTCTGTATTAATCACTTTAGATTCCTAAATACCGAG	180
QY	181	TATGAGTAGGATGATGAGAGCGCAATTCGACTAGAAATGATTCATACATTCCTTAAT	240
Db	181	TATGAGTAGGATGATGAGAGCGCAATTCGACTAGAAATGATTCATACATTCCTTAAT	240
QY	241	CATGATGACCTAACGACGATGATGATGATGATTAATGACAGGAAATTAACAAATCAT	300
Db	241	CATGATGACCTAACGACGATGATGATGATGATTAATGACAGGAAATTAACAAATCAT	300
QY	301	AAAGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	360
Db	301	AAAGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	360
QY	361	GAACTTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	420
Db	361	GAACTTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	420
QY	421	CTGTAAATGACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	480
Db	421	CTGTAAATGACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	480
QY	481	GAAAGCCAAACCAATGATCTTGAATCTTGAATGATGATGATGATGATGATGATGATGATGAT	540
Db	481	GAAAGCCAAACCAATGATCTTGAATCTTGAATGATGATGATGATGATGATGATGATGATGAT	540
QY	541	TTATTAACCTTTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	600
Db	541	TTATTAACCTTTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	600
QY	601	GAACTTATGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	660
Db	601	GAACTTATGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	660
QY	661	TTAGACTGTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	720
Db	661	TTAGACTGTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	720
QY	721	AATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	780
Db	721	AATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	780
QY	781	CATAGAGACGACAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	840
Db	781	CATAGAGACGACAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	840
QY	841	TTATTAAGAAATGCTTGAATTTA 861	
Db	841	TTATTAAGAAATGCTTGAATTTA 861	

RESULT 3  
US-08-781-986A-155/c  
; Sequence 155, Application US/08781986A







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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4184
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4184

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Query Match      55.1%; Score 474; DB 9; Length 864;
Best Local Similarity 99.8%; Pred. No. 6,8e-224;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 16 ATGAATTAATTAATAGATGAAGTCATATGAATTCGGTTCGATTAATTAATGAATGA 75
DB 1 ATGAATTAATTAATAGATGAAGTCATATGAATTCGGTTCGATTAATTAATGAATGA 60
QY 76 ATGATACCTCAGCTAGAGAAAGATGTGTATTCATTAATGCTGAGGTAAAGCCATC 135
DB 61 ATGATACCTCAGCTAGAGAAAGATGTGTATTCATTAATGCTGAGGTAAAGCCATC 120
QY 136 CGACCACTTCCTGATTAATCTCACTTAATTAATTAATTAATTAATTAATTAATTA 195
DB 121 CGACCACTTCCTGATTAATCTCACTTAATTAATTAATTAATTAATTAATTAATTA 180
QY 196 AAGAGCCCAATTCGACATGAAATATTCATCAATTCATTAATTAATTAATTAATTA 255
DB 181 AAGAGCCCAATTCGACATGAAATATTCATCAATTCATTAATTAATTAATTAATTA 240
QY 256 GCGATGATATGATGATTAATTCGACGAGAAATTAATTAATTAATTAATTAATTA 315
DB 241 GCGATGATATGATGATTAATTCGACGAGAAATTAATTAATTAATTAATTAATTA 300
QY 316 TCGACTCGCATTAATGACAGGTGATCTTTTAACTTAACATTTGAATTTGAAGT 375
DB 301 TCGACTCGCATTAATGACAGGTGATCTTTTAACTTAACATTTGAATTTGAAGT 360
QY 376 GATATGATTAATCTGATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 435
DB 361 GATATGATTAATCTGATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
QY 436 GGTATGTTGGAATGTCGCGGCTCAATGTTAGATGCAAAAGCCGCAACCAAT 495
DB 421 GGTATGTTGGAATGTCGCGGCTCAATGTTAGATGCAAAAGCCGCAACCAAT 480
QY 496 GATCTTGAACCTTGGAAATGATACACAAACAGAGAGCA 540
DB 481 GATCTTGAACCTTGGAAATGATACACAAACAGAGAGCA 525

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RESULT 8
US-09-815-242-2822/c
; Sequence 2822, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.

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; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2822
; LENGTH: 413
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-2822

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Query Match      48.0%; Score 413; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 9,6e-194;
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 160 TTGATTCACCTAATTAATCCGATGATGATGATGATGATGATGATGATGATGATG 219
DB 413 TTGATTCACCTAATTAATCCGATGATGATGATGATGATGATGATGATGATGATG 354
QY 220 ATTCAATACCTTCACTTAATTCATGATGATGATGATGATGATGATGATGATGATG 279
DB 353 ATTCAATACCTTCACTTAATTCATGATGATGATGATGATGATGATGATGATGATG 294
QY 280 CGAGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 339
DB 293 CGAGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 234
QY 340 GCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 399
DB 223 GCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 174
QY 400 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 459
DB 173 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 114
QY 460 CAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 519
DB 113 CAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 54
QY 520 CACAAACAAACAAACGAGAGCATTTAATCTTTGCGTTATGATGACAGCAGA 572
DB 53 CACAAACAAACAAACGAGAGCATTTAATCTTTGCGTTATGATGACAGCAGA 1

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RESULT 9
US-10-282-122A-5390/c
; Sequence 5390, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith

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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR FILING DATE: 2003-02-20
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5841
LENGTH: 337
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-10-282-122A-5841

Query Match      39.1%; Score 337; DB 13; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.8e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TACATATTCCTTATTCATGATGACCTACGACGATGATTAAGATGATTAAGAGAG 284
DB 337 TACATATTCCTTATTCATGATGACCTACGACGATGATTAAGATGATTAAGAGAG 278
QY 285 AAAATTAACAATATATAAGATATGATGATGATGATGATTAAGAGATGATCTT 344
DB 277 AAAATTAACAATATATAAGATATGATGATGATGATGATTAAGAGATGATCTT 218
QY 345 ATTAAGTAAGCAATTAAGTATTAAGTATGATTAAGTATTAAGTATTAAGTAAAT 404
DB 217 ATTAAGTAAGCAATTAAGTATTAAGTATGATTAAGTATTAAGTATTAAGTAAAT 158
QY 405 AAAAGTCTACAAAGGCTGCTAATAGCAAGTGTGATGATGATGATGATGATGAT 464
DB 157 AAAAGTCTACAAAGGCTGCTAATAGCAAGTGTGATGATGATGATGATGATGAT 98
QY 465 GTTAGATATGCAAGGCAAGGCAAGCAATGATCTTGAACCTTTGGAATGATACAA 524
DB 97 GTTAGATATGCAAGGCAAGGCAAGCAATGATCTTGAACCTTTGGAATGATACAA 38
QY 525 AACAAAAACAGAGACATTAATTTTGGCGGTATG 561
DB 37 AACAAAAACAGAGACATTAATTTTGGCGGTATG 1
```

```
RESULT 12
US-10-282-122A-34531
Sequence 34531, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 34531
LENGTH: 879
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-10-282-122A-34531

Query Match      2.9%; Score 25; DB 13; Length 879;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 GAGGAAATTAACAATCATTAAGT 305
DB 281 GAGGAAATTAACAATCATTAAGT 305

RESULT 13
US-10-282-122A-17062
Sequence 17062, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
```

```

OY      214  GAAATGATTCATACATATTC 234
|||
Db      226  GAAATGATTCATACATATTC 246

RESULT 15
US-10-369-493-42078
; Sequence 42078, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052) B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ. ID NOS: 47374
; SEQ ID NO 42078
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Lactococcus lactis
US-10-369-493-42078

Query March 2.3%; Score 20; DB 16; Length 858;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Indels 0; Gaps 0;

OY      259  ATGGATATGATGATTATTCG 278
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Db      247  ATGGATATGATGATTATTCG 266

Search completed: April 20, 2004, 11:24:08
Job time : 369 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2004, 05:55:16 / Search time 92 Seconds

(without alignments)  
5193.617 Million cell updates/sec

Title: US-09-925-637-63

Perfect score: 861

Sequence: 1 atgacgaatccatccatgaa.....tattagaatcgtgattta 861

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCUTS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	861	100.0	1893	4	US-08-956-171E-155
2	853	99.1	882	3	US-09-276-873-1
3	449.8	92.2	909	4	US-09-134-001C-334
4	160.4	18.6	939	4	US-09-107-532A-3070
5	157.2	18.3	894	1	US-08-534-910B-5
6	155.6	18.1	893	1	US-08-333-321-1
7	155.6	18.1	894	1	US-08-534-910B-2
8	155.6	18.1	894	1	US-08-534-910B-3
9	155.6	18.1	894	1	US-08-534-910B-4
10	155.6	18.1	894	3	US-08-886-466-1
11	155.6	18.1	894	3	US-09-475-304-1
12	155.6	18.1	894	4	US-09-101-126-4
13	155.6	18.1	894	4	US-09-367-528A-4
14	154	17.9	894	1	US-08-534-910B-1
15	154	17.9	894	4	US-09-367-528A-2
16	150.6	17.5	486	4	US-09-217-609A-28
17	150.6	17.5	486	3	US-08-873-235B-28
18	141	16.4	924	4	US-09-543-681A-1736
19	137	15.9	1664976	4	US-08-916-421B-1
20	136.4	15.8	885	3	US-09-187-050-11
21	134.8	15.7	1173	3	US-09-187-050-13
22	134.8	15.7	1173	3	US-09-187-050-15
23	134.8	15.7	1173	3	US-09-187-050-17
24	134.8	15.7	1173	3	US-09-187-050-19
25	134.8	15.7	1173	3	US-09-187-050-21
26	134.8	15.7	1173	3	US-09-187-050-23
27	134.8	15.7	1173	3	US-09-187-050-25

28	134.8	15.7	1889	3	US-09-187-050-1	Sequence 1, Appl
29	134.4	15.6	847	4	US-09-634-238-85	Sequence 85, Appl
30	131.4	15.3	1830121	4	US-09-557-884-1	Sequence 1, Appl
31	131.4	15.3	1830121	4	US-09-643-990A-1	Sequence 1, Appl
32	124.6	14.5	876	3	US-09-275-742-1	Sequence 76, Appl
33	124.2	14.4	10011	4	US-08-961-527-76	Sequence 692, App
34	117.8	13.7	1029	4	US-09-540-236-692	Sequence 35, Appl
35	117.8	13.7	96109	4	US-09-596-002-35	Sequence 41, Appl
36	114.8	13.3	1914	4	US-09-634-238-41	Sequence 1, Appl
37	114.2	13.3	640681	4	US-09-790-988-1	Sequence 13, Appl
38	98.6	11.5	881	4	US-09-634-903-13	Sequence 64, Appl
39	92.4	10.7	927	4	US-09-328-352-64	Sequence 185, Appl
40	88.6	10.3	884	4	US-08-956-171E-185	Sequence 173, App
41	76.8	8.9	1284	4	US-08-858-207A-173	Sequence 4, Appl
42	72.6	8.4	861	3	US-09-187-050-4	Sequence 7, Appl
43	72	8.4	909	1	US-07-783-705A-7	Sequence 13, Appl
44	72	8.4	6918	1	US-07-783-705A-13	Sequence 1, Appl
45	71.4	8.3	990	1	US-08-410-167A-1	

## ALIGNMENTS

RESULT 1  
US-08-956-171E-155/c  
Sequence 155, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage  
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956, 171E  
FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 155:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1893 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 155:  
US-08-956-171E-155





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QY 29 TAGATGAAGTCAATAATGAATATCGTTGCGATTAATAATCAATATGATCTCAGC 88
DB 80 TACCTGCTGAGAAAAGAAATCTTCTTTTATATAGATACAAAGGATTAAGGAC 139
QY 89 TAGAAGAAGTATGTGTATCTATCAATAAGTGGAGGTAAAGCATCGACAGTTCTGT 148
DB 140 TCTATATAGGAGATGATTTCTGTAAGACAGCGGAAAAGAAATCTCTTATAC 199
QY 149 TATTACTACTTATGATCTAATAATACGATAGTATGTT--AGGTATGAAGCGCA 205
DB 200 TTTTAAAGGCGGCTTCTCTTCTTATGATGAGCCTATGATGTCCCGCTATCAAGTAGCAG 259
QY 206 TTGACACTAGAAATGATTCATACATATTCATTTATATATGATCCACAGAGATGAGA 265
DB 260 CTGCTTTAGAAATGGTGCATACGATATTCCTTGATCCACATGATTTGCTTGCAATGACA 319
QY 266 ATGATGATATTCGACGAGAAATTAACAATCATATAGATATGCTGATGAGTGCAG 325
DB 320 ATGATGATCTTCGAGAGAAAACCTACCATATAGATTCGCGAGAGATTAAGCTA 379
QY 326 TATTAGAGATGATGCTTTATTAATCAATGACATTTGAATTTAATGATGATAGT 385
DB 380 TATTGCGCGAGATGCTTTCTTACAGAGCATTTCCAGCTAAT--CAGTATGGCACACT 436
QY 386 TAACTGATGAAGTAAATAATAAGTCTACAGGCGTCAATAGCAAGTGCATGTG 445
DB 437 TAGGTAATTCCTCTAGAGCTTCTGCTCTTACAGCAATTAGCTGTTGTGGGATCAAG 496
QY 446 GAATGCTCGGCGTCAATGTTAGATATGCAAAAGGAGGCAACCAATTTGATCTTGA 505
DB 497 GTATGCTTGGCGCAAGTGCAGATATCGAGGCGCATGAAAAAGCTTTCTTTAGAG 556
QY 506 CTTTGGAAATGATCAAAAGCAAAAACAGAGCATTTAATCTTTGGGTTATAGTG 565
DB 557 AATTAGATTTATTCATGAAAAGAGAGAGGAGCTTTGATCTTTATGCTTCTGCTG 616
QY 566 CAGCAGATATCGCTAATGCTGATGATCAACTAAGAAACATTTAGAAAGTTATAGTTATC 625
DB 617 GTGCAATATTAAGCAACCACTGAGAAATCTTATGCTACTCAACGATTAAGCCGAA 676
QY 626 ATTTAGATGATGTTCCAGATTTAAAGATTTATTAAGCTGCTATGATGAGAGCA 685
DB 677 ATTTAGATGATGCTTTTCAAGTATGAGATGATCTACGATGATGATGATGATGATG 736
QY 686 AGTAGGTAATAAGTGGGAGCGATCTTGAAAAATAATAAGTACGTACGTAGTTAT 745
DB 737 CATTAAGGAAAACGCTGTTAAGATGACGTATGAAAAATAATCTTACCAGCTTAT 796
QY 746 TAGGAAAAGA 755
DB 797 TAGGCTTAGA 806

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RESULT 5  
US-08-534-910B-5

Sequence 5, Application US/08534910B  
Patent No. 5766911

GENERAL INFORMATION:

APPLICANT: KOIKE, Ayumi

APPLICANT: OBATA, Shusei

APPLICANT: NISHINO, Tokuzo

APPLICANT: OHNODA, Shinichi

APPLICANT: NAKAZAWA, Takeshi

APPLICANT: OGURA, Kyoze

APPLICANT: KOYAMA, Tanetoshi

TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable

TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding Ther

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenyon & Kenyon

STREET: 1025 Connecticut Avenue, N.W., Suite 600

CITY: Washington

```

STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toifeneck, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-5

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Query Match 18.3%; Score 157.2; DB 1; Length 894;  
Best Local Similarity 51.0%; Pred. No. 1.3e-29;  
Matches 400; Conservative 0; Mismatches 378; Indels 6; Gaps 1;

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QY 17 TGAATTAATTAATGATTAATCAATTAATGATGATGATGATTAATTAATCAATTA 76
DB 29 TCAACGACAAAACAGCGGTGGAACAGCGCTCTCCGTTATATAGAGCGCTTAGAG 88
QY 77 TGGATCTCAGCTGAGAAAGATAGTTGTTATTCATTAATAGTGTGAGATTAAGCATCC 136
DB 89 GCGCGCGAAGGTAAAGAGAGATGCGTACTATTTGAGAGCGCGCAACGAAATCC 148
QY 137 GACCAATTCCTGTTATTAATCTTATGATTAATTAATTAATTAATTAATTAATTA 196
DB 149 GTCCCTGCTGCTTCTGCTCAACCGTTCAGGCGCTGCGAAAGACCGGCGATTCG 208
QY 197 AGAGCGCAATTCAGTAAATGATTCATACATATTCATTTATCATGATGATGATGATG 256
DB 209 CCGTCCCTGCGCGCATTAATTAATGATTCATGATCTTTGATCATGATGATGATGATG 268
QY 257 CGATGATTAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 316
DB 269 GCATGGAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 328
QY 317 GACATGCGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 371
DB 329 CGATGCGCAATTCCTGCGCGGAGAGCGGCTTGAAGCTGATGATGATGATGATGATG 388
QY 372 -AAGTATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 430
DB 389 TCGACGATGAGCGCATCCCTCTCCGCTTCGCTCATGCAAGCGCTGCGGAAAG 448
QY 431 CAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490
DB 449 CGCGCGCTCGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
QY 491 CAATGATCTTGAACCTTTGAAATGATACAAACAAAACAGAGAGATTTATTAATCT 550
DB 509 CGCTGACGCTTCGAGAGCTGATATCATTCATGCGCATTAACCGGAAAATGCTCAAT 568

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QY 551 TTGCGTTATGATGACAGATATGCTAATGTCATGATCACTAAGAACTTTAG 610  
 Db 569 ACAGCGTGACACCGCGCTTGTATGCGGCGCTGATGCGCGGAAACGCGGGAGCTTG 628  
 QY 611 AAGTATATGTTATCATTTAGATGATGTTCCAGATTAAGATGATTTAGACTGCT 670  
 Db 629 ACGAATTCGCCCGCATCTTAGGCTTGCTTCAATTCGATGATATTCGATTTG 688  
 QY 671 ATGCTGATGAAGCAAGTTAGTTAAAGTGCGGACGATCTTGAATAATAAAGTA 730  
 Db 689 AAGGGCAGAAAGAAATCGGCAACCGGTGCGCAGCAGCAAGCAACAAAGGCA 748  
 QY 731 CGTACGTGAGTTATTAGGAAAGATGCGGCAAGATTAATGACTTATCTAGAGAG 790  
 Db 749 CGTATCCAGCGTTGCTGCGCTTGCGGCGGCAAGAAAGTTGGCGTTCCATTCGAGG 808  
 QY 791 CAGC 794  
 Db 809 CGGC 812

## RESULT 6

US-08-333-321-1  
 / Sequence 1, Application US/0833321  
 / Patent No. 5786192

## GENERAL INFORMATION:

APPLICANT: Obata, Shushei  
 TITLE OF INVENTION: FARNESYL PYROPHOSPHATE SYNTHETASE  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Edward W. Greason, Esq.  
 STREET: 1 Broadway

CITY: New York

STATE: N.Y.

COUNTRY: U.S.A.

ZIP: 10004

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: NO.5786192epad, Windows 3.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/333,321

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/953,424

FILING DATE: 29-SEP-1992

APPLICATION NUMBER: JP 3-253788

FILING DATE: 01-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Greason, Edward W.

REGISTRATION NUMBER: 18,918

REFERENCE/DOCKET NUMBER: 077670/00310

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 425-7200

TELEFAX: (212) 425-5288

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 893 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Bacillus stearothermophilus

US-08-333-321-1

Query Match 18.1%; Score 155.6; DB 1; Length 893;

Best Local Similarity 50.9%; Pred. No. 3.2e-29;

Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

QY 17 TGAATTAATTATGATGAAAGTCAATATGATTTATGCTTGCATTAATTAATCAAGTAA 76

Db 29 TCAACGACAAAACAGCGGTGAAACAGCGCTCTCCGTTATATAGACGCTTAAG 88  
 QY 77 TGAATCACTAGTAAAGAAATATGTTGTTATTCATTTAAATGCTGAGGTAAACGATCC 136  
 Db 89 GGGCGGAGAACTGAAATAAAGCGATGGCTATCATATGAGGCGCGGCAACGAAATCC 148  
 QY 137 GAACGTTCTGTTATTTACCTTTAGATTCACTAAATACGATATGATGATTAAGTA 196  
 Db 149 GTCCGTGCTGCTTCTCTCCACCGCTTGGCGGCTCGCAAGACCGCGCTCGGATTC 208  
 QY 197 AGAGCGAATTCACATGAATGATTTGATTAATATTAATCACTATTCATGATGACCTAC 256  
 Db 209 CCGTCCGCTGGCGATGAAATGATTCATAGCTCTTTGATCATGATGATTTGCGGA 268  
 QY 257 CGATGATTAATGATGATTTATGACAGAGAAATTAACAAATCAATTAAGTATAGT 316  
 Db 269 GCATGACAAAGATATTTGGGCGGCGCAAGCCGACCAACCAATTAAGTGTTCGCGAG 328  
 QY 317 GACTGCGATTTAGTCAAGTATGCTTTATTAATAAGCATTTGAATTATTC----- 371  
 Db 329 CGATGCGATTTTGGCGGCGGAGCGGTTGTTGACGTACGCGTTTCAATGATCAACGAAA 388  
 QY 372 -AAGTATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430  
 Db 389 TCGACATGACGCGATCCCTCTCCGTCGCGCTTCATGCAACGCTGCGGAAAG 448  
 QY 431 CAATGCTCATGTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490  
 Db 449 CGCGCGGTCGGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508  
 QY 491 CAATGATCTTGAACCTTTGAAATGATGATGATGATGATGATGATGATGATGATGAT 550  
 Db 509 CGTGAAGCTTTGGAAGCTGAAATGATGATGATGATGATGATGATGATGATGATGAT 568  
 QY 551 TTGCGTTATGATGACAGATATGCTAATGTCATGATGATGATGATGATGATGATGAT 610  
 Db 569 ACAGCGTACACCGCGCGCTTGAATGCGCGGCTGATGCCGCGCAACCGGGAGCTTG 628  
 QY 611 AAGTATATGTTATCATTTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 670  
 Db 629 ACGAATTCGCCCGCATCTTAGGCTTGCTTCAATTCGATGATATTCGATTTG 688  
 QY 671 ATGCTGATGAAGCAAGTTAGTTAAAGTGCGGACGATCTTGAATAATAAAGTA 730  
 Db 689 AAGGGCAGAAAGAAATCGGCAACCGGTGCGCAGCAGCAAGCAACAAAGGCA 748  
 QY 731 CGTACGTGAGTTATTAGGAAAGATGCGGCAAGATTAATGACTTATCTAGAGAG 790  
 Db 749 CGTATCCAGCGTTGCTGCGCTTGCGGCGGCAAGAAAGTTGGCGTTCCATTCGAGG 808  
 QY 791 CAGC 794  
 Db 809 CGGC 812

## RESULT 7

US-08-534-9103-2  
 / Sequence 2, Application US/08534910B  
 / Patent No. 5766911

## GENERAL INFORMATION:

APPLICANT: KOIKE, Ayumi

APPLICANT: OBATA, Shushei

APPLICANT: NISHINO, Tokuzo

APPLICANT: OHNUMA, Shinichi

APPLICANT: NAKAZAMA, Takeshi

APPLICANT: OGURA, Kyoze

APPLICANT: KOYAMA, Tanetoshi

TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable

TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding The

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenyon & Kenyon



STREET: 1025 Connecticut Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.  
 ZIP: 20036-5405  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.25" Floppy Disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
 SOFTWARE: IBM/Word Perfect 6.1 Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/534,910B  
 FILING DATE: 28-SEPT-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-25253  
 FILING DATE: 14-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Toffenetti, Judith L.  
 REGISTRATION NUMBER: 39,048  
 REFERENCE/DOCKET NUMBER: 77670/398  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)429-1776  
 TELEFAX: (202)429-0796  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 894 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 ORIGINAL SOURCE:  
 ORGANISM: Bacillus stearothermophilus  
 US-08-534-910B-2

Query Match 18.1%; Score 155.6; DB 1; Length 894;  
 Best Local Similarity 50.9%; Pred. No. 3.2e-29;  
 Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

17 TGAATAATATATAGATGAAGTCAATATATATATCGTTCGATTAATAATCACTA 76  
 29 TCAACGACGAAACAGCGCGTGAACACGCGTCCCGTTATATAGCGCTTGAAG 88  
 77 TGAATACCTAGCTAGAAAGAAAGTATGTTATTCATTAAATGCTGAGGTAAACGATCC 136  
 89 GGGCGGCGAAGGTGAAGAAAGCGATGCGTACTCATTTGAGGCGCGCAACGATCC 148  
 137 GACCAAGTTCGTATTACTGACCTTTAGATTCACTAATACCGAGTATGAGTATGATA 196  
 149 GTCCGTTGCTGCTTCTGTCCACCGTTCAGCGCTTCGCAAAAGCCGCGCTGATTC 208  
 197 AGAGCCGAATGCACTAGAAATGATTATCATATTCATCTATTATTCATGATGACCTAC 256  
 209 CCGTCGCGCTCGCGATGGAATGATCCATACGTACTTTGATCCATGATGATTCGCA 268  
 257 CGATGATATGATGATATGACGACGAGAAATTAACAATCAATAAGATATGAGAT 316  
 269 GCAATGACACGATGATGCGGCGGCGGCAAGCCGACCAACCAATTAAGTTCGCGAGG 328  
 317 GGAAGTGCATATAGCAGGTGATGCTTTATTAATCAATGAATTTGAATTTTC----- 371  
 329 CGATGCGCATCTGGGGGGGAGCGGTTGTGACGTAACGGGTTCAATGATACCGAAA 388  
 372 -AAGTATGATATTAATCTGATGAGTAAATTAATTAAGTTCACAAAGCGCTGCAATG 430  
 389 TCACGATGAGCGATCCCTTCCTTCGCTCGGCTTCGCTCATGCAACGGCTGCGAAG 448  
 431 CAAATGATCATGTTGGAATGTCGCGCGTCAAAATGTTAGATGCAAGGAGCGCAAC 490  
 449 CGGCGGCTCGGAGAGGATGTCGCGCTCAGGACGCGATATGAGAGGAGGAGAAA 508  
 491 CAATGATCTTGAACCTTGAATGATACCAAAACAAACAGAGCTTTTAACTT 550

509 CGCTGACGCTTTGCGAGCTGGAATACATTTCATCGGCAATAAAACCGGAAAAATGCTGCAT 568  
 551 TTGGGTTATAGAGTACAGCAATATTCGCTAATGATGATGATACAACTAAAGACATTTAG 610  
 569 ACAGCGTACAGCGCGCGCTTATGCGCGCGCTGATGCGCGCAACCGGAGCGTTG 628  
 611 AAATTAATGATATCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670  
 629 ACGAATCGCGCGCGCGCGCTTATGCGCGCGCTTATGCGCGCGCTTATGCGCGCGCTTATG 688  
 671 ATGCTGATGAGCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 730  
 689 AAGGGGAGAGAAAGAAATATGCGCAAGCGCGTCCGACGACCAAGCAACAAAGCGA 748  
 731 CGTACGATGATTTATGAGGAAAGATGCGGAGAGATGATGATGATGATGATGATGATGATG 790  
 749 CGTATCAGCGCTTCTGCTTCTGCGCGCGAGAGAAAGTTGCGCTTCATATCGAGG 808  
 791 CAGC 794  
 809 CGGC 812

RESULT 8  
 US-08-534-910B-3  
 Sequence 3, Application US/08534910B  
 Patent No. 5766911  
 GENERAL INFORMATION:  
 APPLICANT: KOIKE, Aynori  
 APPLICANT: OBATA, Shusei  
 APPLICANT: NISHINO, Tokuzo  
 APPLICANT: OHNUMA, Shinichi  
 APPLICANT: NAKAZAWA, Takeshi  
 APPLICANT: OGURA, Kyoza  
 APPLICANT: KOYAMA, Tanetoshi  
 TITLE OF INVENTION: Mutated Farnesylphosphate Synthase Capable  
 TITLE OF INVENTION: Of Synthesizing Geranylgeranylphosphate And Gene Coding The  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kenyon & Kenyon  
 STREET: 1025 Connecticut Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.  
 ZIP: 20036-5405  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.25" Floppy Disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
 SOFTWARE: IBM/Word Perfect 6.1 Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/534,910B  
 FILING DATE: 28-SEPT-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-25253  
 FILING DATE: 14-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Toffenetti, Judith L.  
 REGISTRATION NUMBER: 39,048  
 REFERENCE/DOCKET NUMBER: 77670/398  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)429-1776  
 TELEFAX: (202)429-0796  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 894 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 ORIGINAL SOURCE:  
 ORGANISM: Bacillus stearothermophilus

US-08-534-910B-3

Query Match 18.1%; Score 155.6; DB 1; Length 894;  
 Best Local Similarity 50.9%; Pred. No. 3.2e-29;  
 Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

17 TGAATTAATTAATAGATGAAGTCAATTAATGAATTAATCGGATCGATTAATTAATCAAGTAA 76  
 29 TCAACGAGCAAAACAGCGGTGGAACGCGCTCTCCGTTATTAAGCGCTTAAG 88  
 77 TGAATCTCAGCTAGAGAAAGTATGTATTCATTAATAGCTGAGGTAAAGCATCC 136  
 89 GGCCTGCGAAGCTGAAAAAGCGATGGCTACTCATTTGAGCGCGCGCAACCAATCC 148  
 137 GACCACTTCTGTTATTAATCACTTAATGATCACTAAATCCGATGATGATAGTATGA 196  
 149 GTCCGTTGCTGCTTCTGTCACCGCTTCGCGCGCTCGAAAAAGACCGCGGTGATTGC 208  
 197 AGAGCGCAATTCACACTAGAAATGATTCATACATATTCATTAATGATGACCTACGAG 256  
 209 CCGTGGCTGCGCGATGTAATGATCCATAGCTACTCTTTGATCCATGATGATTTGCCGA 268  
 257 CGATGATTAATGATGATTTGACGACGAAATTAACAATATTAAGTATATGTGAGT 316  
 269 GATGAGCAACATGATTTGCGCGCGCGCAACCGCAACCAATTAAGTTCGCGGAGG 328  
 317 GCACTGCGATTTAGACAGGTGATGCTTTATTAATTAAGCATTTGAATTTTC----- 371  
 329 CGATGGCCATCTTGGCGGGGAGCGGGTTGTAAGTACGCGTTCAATTGATCAACGAAA 388  
 372 -AAGTATGATGATTAATCACTGATGAAGTAAATTAAGTTTACAAAGCGCTGCAATAG 430  
 389 TCGAGCATAGCGCATCCCTCTCTCTCGCGCTTCGCTCATCGAAGCGCTGGGGAAG 448  
 431 CAAGTGTGATGTTGGAATGATCGCGCGGTCAAAATGTTAGTATGCAAGCGAGCCGAC 490  
 449 CGCGCGCTCGGAAAGGATGCGCGCGGTCAAGCGAGCCGATGATGAAAGAGGGAAG 508  
 491 CAATTGATCTTGAACCTTGAATGATACACAAAACAAAACAGAGCATTTATTAATT 550  
 509 CCTGACGCTTTCGAGGCTCGAATCATTCATCGGTATTAACCGGAAAATGCTGCAT 568  
 551 TTGCGGTTATGATGTCAGACGATATCGTAAATGATGATGATCACTAAAGACCTTAG 610  
 569 ACAGCGGTGACGCGCGCGCTTATGCGCGCGCTGATGCGCGCAACCGCGGAGCTTG 628  
 611 AAGTTATAGTATCATTTAGTATGATGATTCAGATTAAGATGATTTATTAAGCTGCT 670  
 629 ACGAATTCGCGCGCATCTAGGCTTGCCTTCAAAATTCGCGATGATTTTCGATATG 688  
 671 ATGCTGATGACCAAGTTAGTAAAGTAAAGTGGCGAGCGATCTTAAATTAATTAAGTA 730  
 689 AAGGGGCAAAACAAAATTCGCGCAAGCGGTGCGAGGACCAACAAACAAAGGA 748  
 731 CGTAGCTGATTTATTAAGGAAAGATGGCGCAGAGATTAATGCTATCATAGAGAG 790  
 749 CGTATCCAGCGCTTGTCTGCTTGCCTGCGGCAAGGAAAGTTCGCTCATATCAGG 808  
 QY 791 CAGC 794  
 DB 809 CGGC 812

RESULT 9  
 US-08-534-910B-4  
 ; Sequence 4; Application US/08534910B  
 ; Patent No. 5766911  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KOIKE, Ayumi  
 ; APPLICANT: OBAI, Shuhei  
 ; APPLICANT: NISHINO, Tokuzo  
 ; APPLICANT: OHMURA, Shiroshi  
 ; APPLICANT: MAKIZAWA, Takeshi

APPLICANT: OGURA, Kyoze  
 TITLE OF INVENTION: Mutated Farnesylphosphate Synthase Capable  
 TITLE OF INVENTION: Of Synthesizing Geranylgeranylphosphate And Gene Coding The  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kenyon & Kenyon  
 STREET: 1025 Connecticut Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.  
 ZIP: 20036-5405  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.25" Floppy Disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
 SOFTWARE: IBM/Word Perfect 6.1 Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/534,910B  
 FILING DATE: 28-SEPT-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-25253  
 FILING DATE: 14-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Toftennet, Judith L.  
 REGISTRATION NUMBER: 39,048  
 REFERENCE/DOCKET NUMBER: 77670/398  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)428-1776  
 TELEFAX: (202)428-0796  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 894 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 ORIGINAL SOURCE:  
 ORGANISM: Bacillus stearothermophilus  
 US-08-534-910B-4

Query Match 18.1%; Score 155.6; DB 1; Length 894;  
 Best Local Similarity 50.9%; Pred. No. 3.2e-29;  
 Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

17 TGAATTAATTAATAGATGAAGTCAATTAATGAATTAATCGGATCGATTAATTAATCAAGTAA 76  
 29 TCAACGAGCAAAACAGCGGTGGAACGCGCTCTCCGTTATTAAGCGCTTAAG 88  
 77 TGAATCTCAGCTAGAGAAAGTATGTATTCATTAATAGCTGAGGTAAAGCATCC 136  
 89 GGCCTGCGAAGCTGAAAAAGCGATGGCTACTCATTTGAGCGCGCGCAACCAATCC 148  
 137 GACCACTTCTGTTATTAATCACTTAATGATCACTAAATCCGATGATGATAGTATGA 196  
 149 GTCCGTTGCTGCTTCTGTCACCGCTTCGCGCGCTCGAAAAAGACCGCGGTGATTGC 208  
 197 AGAGCGCAATTCACACTAGAAATGATTCATACATATTCATTAATGATGACCTACGAG 256  
 209 CCGTGGCTGCGCGATGTAATGATCCATAGCTACTCTTTGATCCATGATGATTTGCCGA 268  
 257 CGATGATTAATGATGATTTGACGACGAAATTAACAATATTAAGTATATGTGAGT 316  
 269 GATGAGCAACATGATTTGCGCGCGCGCAACCGCAACCAATTAAGTTCGCGGAGG 328  
 317 GCACTGCGATTTAGACAGGTGATGCTTTATTAATTAAGCATTTGAATTTTC----- 371  
 329 CGATGGCCATCTTGGCGGGGAGCGGGTTGTAAGTACGCGTTCAATTGATCAACGAAA 388  
 372 -AAGTATGATGATTAATCACTGATGAAGTAAATTAAGTTTACAAAGCGCTGCAATAG 430  
 389 TCGACATGAGCGCATCCCTCTCTCTCGCGCTTCGCTCATCGAAGCGCTGGGGAAG 448  
 QY 389 TCGACATGAGCGCATCCCTCTCTCTCGCGCTTCGCTCATCGAAGCGCTGGGGAAG 448

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QY 431 CAAGTGCATGTTGGAATGCTGGGGTCAATGTTAGATATGCAAGGAGCCAC 490
Db 449 CGGCCGCTCCGGAAGGATGCTGCCGTGAGCCAGCCGATATGAGAGAGGGGAAA 508
QY 491 CAATTGATCTTGAACCTTTGGAATGATACACAAAACAAAACAGAGCATTTAACTT 550
Db 509 CGCTGACGCTTTGAGAGCTGGAATACCTTCATCGGATATAAACCGGAAAATGCTCAAT 568
QY 551 TTGCGGTATGAGTGCAGCAGATATCGCTATATCGATATACAACTAAAGAACTTTG 610
Db 569 ACAGCGTCAAGCGCGGCTTGTATCGCGGCTATATCGCGCAAAACCGGAGCTTG 628
QY 611 AAAGTTAGTTATCATTTAGTATGATGTTCCAGATTAAAGATTATTTAGACTGCT 670
Db 629 ACGAATTCGGCCGCATCTAGGCTTGCTTCAATTCGCGATGATATTCGATATTTG 688
QY 671 ATGCTGATGAAGCAAGTTAGTAAAGAGTGGGCGACCATTTGAAAATTAATTAAGTA 730
Db 689 AAGGGGCAAGAAAGAAATCGGCAAGCGGTCGCGACGACCAACCAACCAAGCA 748
QY 731 CGTACGTGATTTATTAGGAAGATGGCGCAGAAAGTAAATGACTTATCATAGAGAG 790
Db 749 CGATCCAGCGCTTCTGCTTCCGCGCGCAAGAAAGTTGACGTTCCATATGAGG 808
QY 791 CAGC 794
Db 809 CGGC 812

RESULT 10
US-08-886-466-1
; Sequence 1, Application US/08886466C
; Patent No. 6040165
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Narita, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohto, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/08/886,466C
; EARLIER FILING DATE: 1997-07-10
; EARLIER APPLICATION NUMBER: JP 8-191635
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(891)
US-08-886-466-1

Query Match 18.1%; Score 155.6; DB 3; Length 894;
Best Local Similarity 50.9%; Pred. No. 3.2e-29;
Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

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QY 197 AGAGCGCAATTGCACTGAAATGATTCATACATATTCATTTATCATGAGCACTACAG 256
Db 209 CCGTGGCTCGGCGCATTTGAATGATTCATACATGATCTTTGATCATGATGATTTGCCGA 268
QY 257 CGATGATTAATGATGATTTATGACAGAGAAATTTACAAATCATTAAGTATATGAGT 316
Db 269 GCATGACAAAGATGATTTGCGGCGGCGCAAGCCGACGAACCAATTAAGTGTTCGCGAGG 328
QY 317 GCACTGCAATTTAGCAGGTGATGCTTTATTAATTAAGATTTGAATTTTC----- 371
Db 329 CGATGGCCATCTTGGCGGGGACGGGTTGTTGACGTACGGGTTCAATTTGATCACCGAAA 388
QY 372 -AAGTATGATGATTAATCATGATGATGATTAATTAAGTTCTTCAACCGGCTGTCAATAG 430
Db 389 TCGAGATGAGCGCATCCCTCTCTCCGTCGGGCTTCGGCTCATGAAACGGCTGGCGAAAG 448
QY 431 CAAGTGCATGTTGGAATGCTGGCGGCTCAATATGATATGCAAGCGAGCCAC 490
Db 449 CGGCCGCTCCGGAAGGATGCTGCCGCTCAGGACCGCATATGAAAGAGAGGGGAAA 508
QY 491 CAATTGATCTTGAACCTTTGGAATGATACACAAAACAAAACAGAGCATTTAACTT 550
Db 509 CGCTGACGCTTTGAGAGCTGGAATACATTCATCGGCAATAACCGGAAAATGCTGCAAT 568
QY 551 TTGCGGTATGAGTGCAGCAGATATCGCTAATGTCATGATCAACTAAAGAACTTTAG 610
Db 569 ACAGCGTCAAGCGCGGCTTGTATCGCGGCTGATGCGCGCAAAACCGGAGCTTG 628
QY 611 AAAGTTAGTTATCATTTAGTATGATGTTCCAGATTAAAGATTTATAGACTGCT 670
Db 629 ACGAATTCGGCCGCATCTAGGCTTGCTTCAATTCGCGATGATATTCGATATTTG 688
QY 671 ATGCTGATGAAGCAAGTTAGTAAAGAGTGGCGACGATCTTGAATAATTAAGTA 730
Db 689 AAGGGGCAAGAAAGAAATCGGCAAGCGGTCGCGACGACCAACCAACCAAGCA 748
QY 731 CGTACGTGATTTATTAGGGAAGATGGCGCAGAAAGTAAATGACTTATCATAGAGAG 790
Db 749 CGATCCAGCGCTTCTGCTTCCGCGCGCAAGAAAGTTGCGCTTCCATATGAGG 808
QY 791 CAGC 794
Db 809 CGGC 812

RESULT 11
US-09-475-304-1
; Sequence 1, Application US/09475304
; Patent No. 6225096
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Narita, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohto, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/09/475,304
; EARLIER FILING DATE: 1999-12-30
; EARLIER APPLICATION NUMBER: JP 8-191635
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(891)
US-09-475-304-1

```

Query Match 18.1%; Score 155.6; DB 3; Length 894;  
 Best Local Similarity 50.9%; Pred. No. 3.2e-29;  
 Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

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QY 17 TGAATTAATTAATAGATGAAGTCAATTAATGAATTAATCGGTGCGATTAATAATACATGA 76
DB 29 TCAACGAGCAAAAACGCGGTGGAACACGCGCTCTCCGTTATATAGAGCGCTTGAAG 88
QY 77 TGAATTAATTAATAGATGAAGTCAATTAATGAATTAATCGGTGCGATTAATAATACATGA 136
DB 89 GGCAGGCGAAGTGAAGAAAGGCGATGCGTACTCAATTAATGAGCGCGCAACCAATCC 148
QY 137 GACCAATGCTTATTAATCACTTATGATTAATCACTTAATCACTTAATGAGTATGATGA 196
DB 149 GTCCGTTGCTGCTTCTGTCACCGCTTCGCGCGCTCGGCAAAAGCCGCGCTCGGATTGC 208
QY 197 AGAGCGCAATTCGACTAGAAATGATTCATACATTAATCACTTAATGATGATGATGATGATG 256
DB 209 CGGTGCGCTGCGGATTAATGATTCATACGTAATCTTGTATGATGATGATGATGATGATGATG 268
QY 257 CGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 316
DB 269 GCAATGACAAAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 328
QY 317 GCACTGCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 371
DB 329 CGATGCGCAATTCGACTAGAAATGATTCATACATTAATCACTTAATGATGATGATGATGATG 388
QY 372 -AAGTATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 430
DB 389 TCGACGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 448
QY 431 CAAGTATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 490
DB 449 CGGCGCTGCGGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 508
QY 491 CAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 550
DB 509 CGGTGCGCTGCGGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 568
QY 551 TTGCGCTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 610
DB 569 ACAGCGTGAAGCGCGGCTTGAATGATTAATGATTAATGATTAATGATTAATGATTAATG 628
QY 611 AAATTAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 670
DB 629 ACGAATTCGCGCGCATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 688
QY 671 ATGATTAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 730
DB 689 AAGGCGCAAGAAAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 748
QY 731 CGTACGTAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 790
DB 749 CGTATCCAGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
QY 791 CAGC 794
DB 809 CGGC 812

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RESULT 12  
 us-09-101-126-4

Sequence 4, Application US/09101126  
 Patent No. 6316216  
 GENERAL INFORMATION:  
 APPLICANT: OHTO, CHIKARA  
 APPLICANT: NAKANE, HIROYUKI  
 APPLICANT: NISHIKI, TOKUO  
 APPLICANT: OHNUMA, SHINICHI  
 APPLICANT: HIROOKA, KAZUTAKE  
 TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES

FILE REFERENCE: 77670/566  
 CURRENT APPLICATION NUMBER: US/09/101,126  
 CURRENT FILING DATE: 1999-04-27  
 EARLIER APPLICATION NUMBER: PCT/JP97/03921  
 EARLIER FILING DATE: 1997-10-29  
 EARLIER APPLICATION NUMBER: JP 8-307506  
 EARLIER FILING DATE: 1996-11-05  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: Patentm Ver. 2.0  
 SEQ ID NO 4  
 LENGTH: 894  
 TYPE: DNA  
 ORGANISM: Bacillus stearothermophilus  
 FEATURE:  
 OTHER INFORMATION: 256-276 is an Asp-rich coding domain  
 us-09-101-126-4

Query Match 18.1%; Score 155.6; DB 4; Length 894;  
 Best Local Similarity 50.9%; Pred. No. 3.2e-29;  
 Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

```

QY 17 TGAATTAATTAATAGATGAAGTCAATTAATGAATTAATCGGTGCGATTAATAATACATGA 76
DB 29 TCAACGAGCAAAAACGCGGTGGAACACGCGCTCTCCGTTATATAGAGCGCTTGAAG 88
QY 77 TGAATTAATTAATAGATGAAGTCAATTAATGAATTAATCGGTGCGATTAATAATACATGA 136
DB 89 GGCAGGCGAAGTGAAGAAAGGCGATGCGTACTCAATTAATGAGCGCGCAACCAATCC 148
QY 137 GACCAATGCTTATTAATCACTTATGATTAATCACTTAATCACTTAATGAGTATGATGA 196
DB 149 GTCCGTTGCTGCTTCTGTCACCGCTTCGCGCGCTCGGCAAAAGCCGCGCTCGGATTGC 208
QY 197 AGAGCGCAATTCGACTAGAAATGATTCATACATTAATCACTTAATGATGATGATGATGATGATG 256
DB 209 CGGTGCGCTGCGGATTAATGATTCATACGTAATCTTGTATGATGATGATGATGATGATGATG 268
QY 257 CGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 316
DB 269 GCAATGACAAAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 328
QY 317 GCACTGCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 371
DB 329 CGATGCGCAATTCGACTAGAAATGATTCATACATTAATCACTTAATGATGATGATGATGATG 388
QY 372 -AAGTATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 430
DB 389 TCGACGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 448
QY 431 CAAGTATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 490
DB 449 CGGCGCTGCGGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 508
QY 491 CAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 550
DB 509 CGGTGCGCTTTCGAGCTGGAATTAATCATCATGCGGCAATTAATCGGGAATTCGTCAT 568
QY 551 TTGCGCTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 610
DB 569 ACAGCGTGAAGCGCGGCTTGAATGATTAATGATTAATGATTAATGATTAATGATTAATG 628
QY 611 AAATTAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 670
DB 629 ACGAATTCGCGCGCATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 688
QY 671 ATGATTAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 730
DB 689 AAGGCGCAAGAAAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 748
QY 731 CGTACGTAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 790
DB 749 CGTATCCAGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808

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QY 791 CAGC 794  
DB 809 CGGC 812

## RESULT 13

US-09-367-528A-4  
Sequence 4, Application US/09367528A  
Patent No. 6395525  
GENERAL INFORMATION:  
APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA  
TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene  
FILE REFERENCE: PH-586  
CURRENT APPLICATION NUMBER: US/09/367,528A  
CURRENT FILING DATE: 1999-08-16  
PRIORITY APPLICATION NUMBER: JP97/346686  
PRIORITY FILING DATE: 1997-12-16  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 894  
TYPE: DNA  
ORGANISM: Bacillus stearothermophilus  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (1)..(894)  
US-09-367-528A-4

Query Match 18.1%; Score 155.6; DB 4; Length 894;  
Best Local Similarity 50.8%; Pred. No. 3,2e-29;  
Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

QY 17 TGAATAATTATAGATGAAGTCAATATGATATCGTTGCGATTAATTAATCACTAA 76  
DB 29 TCAACGACAAACACAGCCGCTGGAACAGCGCTCCCTATATAGACCGCTTAGAAG 88  
QY 77 TGAATCTCAGCTAGAAAGAAATGTTGTTATTCATTAAATGCTGAGAGTAACGATCC 136  
DB 89 GGGCGGGAAGCTGAAAGAGCGGATGCGTACATCTGATGAGCGCGGGAACGATCC 148  
QY 137 GACCAATCTGTATTAATCACTTAATTAATCACTTAATCACTTAATCACTTAATCA 196  
DB 149 GTCCGTGCTGCTCTCTGCAACCGTTGGGGCGCTCGGCAAGACCGCGGCTGGAATTG 208  
QY 197 AGACGCAATTCAGTAAATGATTAATCAATTAATCAATTAATCAATTAATCAAT 256  
DB 209 CCGTGGCTGGCGATTAATGATCAATCAATCAATCAATCAATCAATCAATCAAT 268  
QY 257 CGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 316  
DB 269 GCAATGACAAAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 328  
QY 317 GGAATGCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 371  
DB 329 CGATGCGCATCTTGGCGGGAACGCGTGTGATGATGATGATGATGATGATGATGAT 388  
QY 372 -AAGTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 430  
DB 389 TCGACGATGACGATCCCTCTCCCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCG 448  
QY 431 CAAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 490  
DB 449 CGCGCGGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508  
QY 491 CAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 550  
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QY 551 TTGGCGTATGATGACGACGATTAATGATTAATGATTAATGATTAATGATTAATGAT 610  
DB 569 AAGAGTGCACGCGCGGCTGATCGCGCGGCTGATCGCGCGGCTGATCGCGCGGCTGAT 628  
QY 611 AAGTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 670

DB 629 ACGAATTCGCCGCCATCTAGGCTTGCCTTCAATTCGCGATGATTAATCTGATATTG 688  
QY 671 ATGGTATGAAGCAAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 730  
DB 689 AAGGGGCAAGAAAGAAATCGGCAAGCCGCTCGGCAACGACCAAGCAACCAAGCGA 748  
QY 731 CCTACGTGATTTATTTAGGGAAGATGCGCGCAAGATTAATTAATTAATTAATTAAT 790  
DB 749 GATATTCAGCGCTTCTGCTGCTTCCCGCGCGAAGAAAGTTGCGCTTCAATTCGAG 808  
QY 791 CAGC 794  
DB 809 CGGC 812

## RESULT 14

US-08-534-910B-1  
Sequence 1, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyozo  
APPLICANT: KOYAMA, Tanetsuchi  
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl diphosphate And Gene Coding The  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC

COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEP-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Tofenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 894 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-1

Query Match 17.9%; Score 154; DB 1; Length 894;  
Best Local Similarity 50.8%; Pred. No. 7.8e-29;  
Matches 398; Conservative 0; Mismatches 380; Indels 6; Gaps 1;

QY 17 TGAATAATTATAGATGAAGTCAATATGATTAATGATTAATGATTAATGATTAAT 76

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Db      29 TCAACGAGCAAAAACAGCGGTGAGAAACAGCGCTCTCCCGTTATATATAGCGCTTAGAG 88
Qy      77 TGGATATCTAGCTAGAGAAAGATATGTTGATTCATTAATAGCTGAGGTAACGATCC 136
Db      89 GCGCGGCGAAGCTGAAAAAGCGATGGCGTACTCATTTGAGGCGCGGCAACGAAATCC 148
Qy      137 GACCGATCTGTATATCTACTTATAGATACACTAAATACGAGATAGATAGTAGTATGA 196
Db      149 GTCCGTGCTGCTTCTGCTCCACCGTTGCGGCGCTGAGAAAACCCGCGCTGCAATTGC 208
Qy      197 AGAGCGCAATTCACACTAGAAATGATTCATACATATTCATTAATGATGACCTACAG 256
Db      209 CCGTCGCGCTGCGGATGAAATGATTCATACGACACTCTTTGATTCATGATGATTTGCCGA 268
Qy      257 CGATGATATATGATATTTATCGACGAGGAAATTAACAATCATATAATATATATGTTAGT 316
Db      269 GCAATGACACAGATGATTTGCGCGCGGCAAGCCGACGACAAACAAATGATTTGCGGAGG 328
Qy      317 GCACTGCGATATTAGCAGGTGATGCTTTATTAATTAAGCAATTTGAATTTTC----- 371
Db      329 CGATGCGCATCTTGGCGGGGAGCGGGTGTGACGTACGCTTCAATTCATTCACCGGAA 388
Qy      372 -AAGTATGATATGATTAATGATGAATGAAAAATTAAGTTTACACGCGCTGTCAATAG 430
Db      389 TCGACGATGACGCAATCCCTCCCTCCGTCGCGCTTCATCGAACGCGTGGCGAAAG 448
Qy      431 CAATGATGATGTTGGAATGATCGAGGGTCAAAATGTTAGATGCAAAAGCGAAGCCAC 490
Db      449 CCGCGCGTCCGAGAGGATGATCGCGGTGAGCGGACCGATGAGAAAGAGGAGGAAA 508
Qy      491 CAATGATCTTGAACCTTTGAAATGATACACAAAACAAAACAGAGCAATTAATTAAT 550
Db      509 CCGTACGCTTTGAGAGCTCGAATCATTCATTCGCGATTAACCGGAAAATGCTGCAT 568
Qy      551 TTGCGGTTATGATGACAGATATCGCTAATGATGATGATCACTAAAGAACTTAG 610
Db      569 ACAGCGTGACCGCGCGCTTGAATCGCGGCGTGATGCGCGCAACCGCGGAGCTTG 628
Qy      611 AAAGTTATAGTTATCATTTAGATGATGATTCAGATTAAGATTAATTAATTAAGCTCT 670
Db      629 ACGAATTCGCGCGCATCTAGGCTTGCCTTTCAATTCGCGATGATTTCCGATATG 688
Qy      671 ATGTGATGAAGCAAAAGTTAGTAAAAAGTGGCGAGGATTTGAAAATTAATTAAGTA 730
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Qy      731 CGTACGTGATTTATTAAGGAAAGATGGCGCAGAAATTAATTAATTAATTAATTAAG 790
Db      749 CGTATCCAGCGTTGCTGCTGCTTGCAGGCGAAGAAAAGTTGCGCTTCCATTCGAGG 808
Qy      791 CAGC 794
Db      809 CGGC 812

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## RESULT 15

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US-09-367-528A-2
; Sequence 2, Application US/09367528A
; Patent No. 6395525
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diposphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 894
; TYPE: DNA

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ORGANISM: Bacillus stearothermophilus

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(894)

US-09-367-528A-2

## Query Match

17.9%; Score 154; DB 4; Length 894;

Best Local Similarity 50.8%; Pred. No. 7,8e-29;

Matches 398; Conservative 0; Mismatches 380; Indels 6; Gaps 1;

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Qy      77 TGGATATCTAGCTAGAGAAAGATATGTTGATTCATTAATAGCTGAGGTAACGATCC 136
Db      89 GCGCGGCGAAGCTGAAAAAGCGATGGCGTACTCATTTGAGGCGCGGCAACGAAATCC 148
Qy      137 GACCGATCTGTATATCTACTTATAGATACACTAAATACGAGATAGATAGTAGTATGA 196
Db      149 GTCCGTGCTGCTTCTGCTCCACCGTTGCGGCGCTGAGAAAACCCGCGCTGCAATTGC 208
Qy      197 AGAGCGCAATTCACACTAGAAATGATTCATACATATTCATTAATGATGACCTACAG 256
Db      209 CCGTCGCGCTGCGGATGAAATGATTCATACGACACTCTTTGATTCATGATGATTTGCCGA 268
Qy      257 CGATGATATGATATTTATCGACGAGGAAATTAACAATCATATAATATATATGTTAGT 316
Db      269 GCAATGACACAGATGATTTGCGCGCGGCAAGCCGACGACAAACAAATGATTTGCGGAGG 328
Qy      317 GCACTGCGATATTAGCAGGTGATGCTTTATTAATTAAGTTTACACGCGCTGTCAATAG 430
Db      329 CGATGCGCATCTTGGCGGGGAGCGGGTGTGACGTACGCTTCAATTCATTCACCGGAA 448
Qy      372 -AAGTATGATATGATTAATGATGAATGAAAAATTAAGTTTACACGCGCTGTCAATAG 490
Db      389 TCGACGATGACGCAATCCCTCCCTCCGTCGCGCTTCATCGAACGCGTGGCGAAAG 508
Qy      431 CAATGATGATGTTGGAATGATCGAGGGTCAAAATGTTAGATGCAAAAGCGAAGCCAC 550
Db      449 CCGCGCGTCCGAGAGGATGATCGCGGTGAGCGGACCGATGAGAAAGAGGAGGAAA 568
Qy      491 CAATGATCTTGAACCTTTGAAATGATACACAAAACAAAACAGAGCAATTAATTAAT 550
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Qy      551 TTGCGGTTATGATGACAGATATCGCTAATGATGATGATCACTAAAGAACTTAG 610
Db      569 ACAGCGTGACCGCGCGCTTGAATCGCGGCGTGATGCGCGCAACCGCGGAGCTTG 628
Qy      611 AAAGTTATAGTTATCATTTAGATGATGATTCAGATTAAGATTAATTAATTAAGCTCT 670
Db      629 ACGAATTCGCGCGCATCTAGGCTTGCCTTTCAATTCGCGATGATTTCCGATATG 688
Qy      671 ATGTGATGAAGCAAAAGTTAGTAAAAAGTGGCGAGGATTTGAAAATTAATTAAGTA 730
Db      689 AAGGGGCAAGAAAAAATCGGCAAGCCGCTGCGACGACCAAAACAAACAAAGCGA 748
Qy      731 CGTACGTGATTTATTAAGGAAAGATGGCGCAGAAATTAATTAATTAATTAATTAAG 790
Db      749 CGTATCCAGCGTTGCTGCTGCTTGCAGGCGAAGAAAAGTTGCGCTTCCATTCGAGG 808
Qy      791 CAGC 794
Db      809 CGGC 812

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 Job time : 115 secs

Tue Apr 20 12:43:38 2004

us-09-925-637-63\_1.rnpb

Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2004, 06:54:36 ; Search time 415 seconds  
(without alignments)  
9283.408 Million cell updates/sec

Title: US-09-925-637-63  
Perfect score: 861  
Sequence: 1 atgcagcaatctaccgcatgaa.....tattagaatcgttgattta 861

Scoring table:  
Gapop 10.0 , Gapext 1.0

Searched: 2890132 seqs, 2237290429 residues  
Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	861	100.0	861	9	US-09-925-637-63
2	861	100.0	861	15	US-10-084-205-63
3	861	100.0	1893	8	US-08-781-986A-155
4	861	100.0	1893	13	US-10-329-624-155
5	854.6	99.3	882	13	US-10-282-122A-8179
6	846.6	96.6	882	9	US-09-815-242-8485
7	831.6	96.6	864	9	US-09-815-242-4184
8	449.8	52.2	879	13	US-10-282-122A-34531
9	444.2	51.6	879	13	US-10-282-122A-35068
10	413	48.0	413	9	US-09-815-242-2822
11	413	48.0	413	13	US-10-282-122A-5390
12	337	39.1	337	9	US-09-815-242-3275
13	337	39.1	337	13	US-10-282-122A-5841
14	252.6	29.3	882	13	US-10-282-122A-24756

15	239.8	27.9	5635	16	US-10-398-221-3823	Sequence 3823, Ap
16	231.2	26.9	495269	16	US-10-398-221-8	Sequence 8, Appl
17	231.2	26.9	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
18	227.6	26.7	882	13	US-10-282-122A-1652	Sequence 1652, A
19	227.6	26.7	882	13	US-10-282-122A-17062	Sequence 17062, A
20	220	25.6	891	16	US-10-369-493-40236	Sequence 40236, A
21	218.6	25.4	885	16	US-10-369-493-41045	Sequence 41045, A
22	214.6	24.9	870	13	US-10-282-122A-15342	Sequence 15342, A
23	213.6	24.8	888	13	US-10-282-122A-9306	Sequence 9306, Ap
24	198.4	23.0	879	13	US-10-282-122A-21105	Sequence 21105, A
25	196.8	22.9	882	9	US-09-815-242-6533	Sequence 6533, Ap
26	195	22.6	7528	9	US-09-070-927A-55	Sequence 55, Appl
27	175.2	20.3	873	13	US-10-282-122A-38458	Sequence 38458, A
28	174.8	20.3	858	16	US-10-369-493-42078	Sequence 42078, A
29	174.4	20.3	783	16	US-10-369-493-33397	Sequence 33397, A
30	164	19.0	811	9	US-09-974-300-1015	Sequence 1015, Ap
31	163.2	19.0	927	16	US-10-369-493-42439	Sequence 42439, A
32	161.2	18.7	819	16	US-10-369-493-46888	Sequence 46888, A
33	155.6	18.1	894	13	US-10-462-698A-75	Sequence 75, Appl
34	151.6	17.6	795	13	US-10-282-122A-21259	Sequence 21259, A
35	150.6	17.5	930	16	US-10-369-493-43609	Sequence 43609, A
36	150.2	17.4	888	16	US-10-369-493-24167	Sequence 24167, A
37	142.6	16.6	921	13	US-10-282-122A-32509	Sequence 32509, A
38	142.2	16.5	867	13	US-10-282-122A-36078	Sequence 36078, A
39	141.6	16.4	888	16	US-10-369-493-44860	Sequence 44860, A
40	138	16.0	870	16	US-10-369-493-44580	Sequence 44580, A
41	137	15.9	984	16	US-10-369-493-45179	Sequence 45179, A
42	134.6	15.6	888	13	US-10-282-122A-30834	Sequence 30834, A
43	134.4	15.6	847	16	US-10-264-213-81	Sequence 81, Appl
44	134.4	15.6	5805	16	US-10-264-213-116	Sequence 116, Ap
45	131.4	15.3	888	9	US-09-815-242-7142	Sequence 7142, Ap

#### ALIGNMENTS

RESULT 1  
US-09-925-637-63  
Sequence 63, Application US/09925637  
Patent No. US2002010338A1  
GENERAL INFORMATION:  
APPLICANT: ChOI  
TITLE OR INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides  
FILE REFERENCE: PB560  
CURRENT APPLICATION NUMBER: US/09/925, 637  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/23773  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US 60/151,933  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: US 08/781,986  
PRIOR FILING DATE: 1997-01-03  
PRIOR APPLICATION NUMBER: US 08/956,171  
PRIOR FILING DATE: 1997-10-20  
PRIOR APPLICATION NUMBER: US 60/009,861  
PRIOR FILING DATE: 1996-01-06  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 63  
LENGTH: 861  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-637-63  
Query Match 100.0%; Score 861; DB 9; Length 861;  
Best Local Similarity 100.0%; Pred. No. 1.7e-177;  
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGACGATCTACCGATGAATTAATTAATGAAGTCAATTAATTAATGCGTTCG 60  
Db 1 ATGACGATCTACCGATGAATTAATTAATGAAGTCAATTAATTAATGCGTTCG 60  
QY 61 AATAAATAACGATTAATGATCTACGCTAGAGAAAGATGTGTGATTCATTAATGCT 120



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Db      61  ATAAATTAATCAGTAATGATGACTCAGTAGAAGAAAGATGTTGATTCATTAATGCT 120
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Db      121  GAGAGTAACGCAATCCGACAGTCTGTATATACACTTGAATTCATTAATGCT 180
QY      181  TATGAGTTAGGTATGAAGACGCAATGCACTAAGAAATGATTCATTAATGCT 240
Db      181  TATGAGTTAGGTATGAAGACGCAATGCACTAAGAAATGATTCATTAATGCT 240
QY      241  CATGATGACCTACCAAGATGATTAATGATTAATGATTAATGATTAATGAT 300
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QY      361  GAATCTATTTCAAGTATGATTAATGATTAATGATTAATGATTAATGAT 420
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QY      421  CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGAT 480
Db      421  CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGAT 480
QY      481  GAAAGCCCAACCAATGATCTTGAACCTTGAAGATGATGATGATGATGAT 540
Db      481  GAAAGCCCAACCAATGATCTTGAACCTTGAAGATGATGATGATGATGAT 540
QY      541  TTAATTAATCTTGGGTTATGATGATGATGATGATGATGATGATGATGAT 600
Db      541  TTAATTAATCTTGGGTTATGATGATGATGATGATGATGATGATGATGAT 600
QY      601  GAAATTTAGAAAGTATGATTAATGATTAATGATTAATGATTAATGAT 660
Db      601  GAAATTTAGAAAGTATGATTAATGATTAATGATTAATGATTAATGAT 660
QY      661  TTGACATGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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QY      721  AATTAAGTACGTAAGTATGATTAATGATTAATGATTAATGATTAATGAT 780
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QY      781  CATGAGACGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 840
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Db      841  TTATTAAGAAATCGTTGATTTA 861
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RESULT 2
US-10-084-205-63
; Sequence 63, Application US/10084205
; Publication No. US20030049648A1
; GENERAL INFORMATION:
; APPLICANT: Choi, G.H.
; TITLE OR INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: P815P1
; CURRENT APPLICATION NUMBER: US/10/084,205
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 63
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; LENGTH: 861
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-084-205-63
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Query Match      100.0%; Score 861; DB 15; Length 861;
Best Local Similarity 100.0%; Pred. No. 1.7e-177;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      61  ATAAATTAATCAGTAATGATGACTCAGTAGAAGAAAGATGTTGATTCATTAATGCT 120
QY      121  GAGAGTAACGCAATCCGACAGTCTGTATATACACTTGAATTCATTAATGCT 180
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Db      361  GAATCTATTTCAAGTATGATTAATGATTAATGATTAATGATTAATGAT 420
QY      421  CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGAT 480
Db      421  CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGAT 480
QY      481  GAAAGCCCAACCAATGATCTTGAACCTTGAAGATGATGATGATGATGAT 540
Db      481  GAAAGCCCAACCAATGATCTTGAACCTTGAAGATGATGATGATGATGAT 540
QY      541  TTAATTAATCTTGGGTTATGATGATGATGATGATGATGATGATGATGAT 600
Db      541  TTAATTAATCTTGGGTTATGATGATGATGATGATGATGATGATGATGAT 600
QY      541  TTAATTAATCTTGGGTTATGATGATGATGATGATGATGATGATGATGAT 600
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QY      781  CATGAGACGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db      781  CATGAGACGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY      841  TTATTAAGAAATCGTTGATTTA 861
Db      841  TTATTAAGAAATCGTTGATTTA 861
```

```
RESULT 3
US-08-781-986A-155/C
; Sequence 155, Application US/08781986A
```



Publication No. US20030054436A1  
 GENERAL INFORMATION:  
 APPLICANT: Charles Kunsch  
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
 NUMBER OF SEQUENCES: 5255  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/781,986A  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Benson, Bob  
 REGISTRATION NUMBER: 30,446  
 REFERENCE/DOCKET NUMBER: PB248BP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 155:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1893 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 US-08-781-986A-155

Query Match 100.0%; Score 861; DB 8; Length 1893;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-177;  
 Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCAATCTACCGCATGAATTAATTAATGATGAGTCATTAATGATTCGCTGGC 60  
 DB 1314 ATGAGCAATCTACCGCATGAATTAATTAATGATGAGTCATTAATGATTCGCTGGC 1255

QY 61 ATAAATAATCATGTAATGATGATCTAGCTAGAGAAAGTATGTTGATTCATTAATGCT 120  
 DB 1254 ATAAATAATCATGTAATGATGATCTAGCTAGAGAAAGTATGTTGATTCATTAATGCT 1195

QY 121 GGAGGTAAACGATCCGACCAAGTTCTGTATTAATCTACTTATGATTCATTAATACCGAG 180  
 DB 1194 GGAGGTAAACGATCCGACCAAGTTCTGTATTAATCTACTTATGATTCATTAATACCGAG 1135

QY 131 TATGATGATGATTAAGAGCGCAATTCGACTAGAAAGTATTCATTAATGATTCATTAAT 240  
 DB 1134 TATGATGATGATTAAGAGCGCAATTCGACTAGAAAGTATTCATTAATGATTCATTAAT 1075

QY 241 CATGATGACCTACCGCATGATGATGATGATTAATTCAGACGAGAAATTAACCAATCAT 300  
 DB 1074 CATGATGACCTACCGCATGATGATGATGATTAATTCAGACGAGAAATTAACCAATCAT 1015

QY 301 AAAGTATGATGATGATGATGATGATGATTAATTCAGACGATGATGATTAATTCAGACGAT 360  
 DB 1014 AAAGTATGATGATGATGATGATGATGATTAATTCAGACGATGATGATTAATTCAGACGAT 955

QY 361 GAACCTATTTCAAGTATGATGATTAATTCAGATGATGATTAATTAATTAATTAATTAATTA 420  
 DB 954 GAACCTATTTCAAGTATGATGATTAATTCAGATGATGATTAATTAATTAATTAATTAATTA 895

QY 421 CTGTCAATGACGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

DB 894 CTGTCAATGACGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835  
 QY 481 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
 DB 834 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 775  
 QY 541 TTATTAATCTTTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 DB 774 TTATTAATCTTTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715

QY 601 GAACATTGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 DB 714 GAACATTGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655

QY 661 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
 DB 654 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595

QY 721 AATTAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 DB 594 AATTAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 535

QY 781 CATAGAGCGCAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 DB 534 CATAGAGCGCAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475

QY 841 TTATTAGAAATCGTTGATTTA 861  
 DB 474 TTATTAGAAATCGTTGATTTA 454

RESULT 4  
 US-10-329-624-155/c  
 Sequence 155, Application US/10329624  
 Publication No. US20040043037A1  
 GENERAL INFORMATION:  
 APPLICANT: Charles Kunsch  
 Gil H. Choi  
 Patrick S. Dillon  
 Craig A. Rosen  
 Steven C. Barash  
 Michael R. Fannon  
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
 NUMBER OF SEQUENCES: 5256  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/329,624  
 FILING DATE: 27-Dec-2002  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/956,171  
 FILING DATE: October 20, 1997  
 APPLICATION NUMBER: 66/009,861  
 FILING DATE: January 5, 1996  
 APPLICATION NUMBER: 08/781,986  
 FILING DATE: January 3, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mark J. Hyman  
 REGISTRATION NUMBER: 46,789  
 REFERENCE/DOCKET NUMBER: PB248P1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (240) 314-1224  
 TELEFAX: (301) 309-8439

```

; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1893 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 155:
US-10-329-624-155

Query Match      100.0%; Score 861; DB 13; Length 1893;
Best Local Similarity 100.0%; Pred. No. 2.3e-177;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGAATCTACCGATGGAATTAATTAATAGATGAAGTCAATATGATTAATGCGTTGCG 60
DB 1314 ATGACGAATCTACCGATGGAATTAATTAATAGATGAAGTCAATATGATTAATGCGTTGCG 1255

QY 61 ATAAATTAATCAGTAATGTAATCTACGCTAGAAAGAAAGTGTGTATTCATTAATGCT 120
DB 1254 ATAAATTAATCAGTAATGTAATCTACGCTAGAAAGAAAGTGTGTATTCATTAATGCT 1195

QY 121 GGAGTAAACGATCCGACAGTTCTGTATTCTCACTTATAGATTCACTAATACCGAG 180
DB 1194 GGAGTAAACGATCCGACAGTTCTGTATTCTCACTTATAGATTCACTAATACCGAG 1135

QY 181 TATGAGTTAGGTATGAAGACCAATTGCACTAGAAAATGATTCATATTCATTTACTTAT 240
DB 1134 TATGAGTTAGGTATGAAGACCAATTGCACTAGAAAATGATTCATATTCATTTACTTAT 1075

QY 241 CATGATGACCTACCGAGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 300
DB 1074 CATGATGACCTACCGAGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 1015

QY 301 AAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 1014 AAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955

QY 361 GAATCTATTTCAAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 954 GAATCTATTTCAAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 895

QY 421 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 894 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835

QY 481 GAAGGCCAACCAATTGATCTTGAACCTTGGAAATGATACACAAAACAAAACAGAGACA 540
DB 834 GAAGGCCAACCAATTGATCTTGAACCTTGGAAATGATACACAAAACAAAACAGAGACA 775

QY 541 TTATTAATCTTTGCGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 774 TTATTAATCTTTGCGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715

QY 601 GAACATTTAGAAAGTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
DB 714 GAACATTTAGAAAGTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 655

QY 661 TTAGACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 654 TTAGACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595

QY 721 AATTAAGTACGTAAGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
DB 594 AATTAAGTACGTAAGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 535

QY 781 CATAGAGACGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 534 CATAGAGACGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475

QY 841 TTATTAAGAAATCGTTGATTTA 861
DB 474 TTATTAAGAAATCGTTGATTTA 454

```

```

RESULT 5
US-10-282-122A-8179
; Sequence 8179, Application US/10282122A
; Publication No. US20040029125A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EPIYA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8179
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-282-122A-8179

Query Match      99.3%; Score 854.6; DB 13; Length 882;
Best Local Similarity 99.5%; Pred. No. 4.2e-176;
Matches 857; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGACGAATCTACCGATGGAATTAATTAATAGATGAAGTCAATATGATTAATGCGTTGCG 60
DB 1 ATGACGAATCTACCGATGGAATTAATTAATAGATGAAGTCAATATGATTAATGCGTTGCG 60

QY 61 ATAAATTAATCAGTAATGTAATCTACGCTAGAAAGAAAGTGTGTATTCATTAATGCT 120
DB 61 ATAAATTAATCAGTAATGTAATCTACGCTAGAAAGAAAGTGTGTATTCATTAATGCT 120

QY 121 GGAGTAAACGATCCGACAGTTCTGTATTCTCACTTATAGATTCACTAATACCGAG 180
DB 121 GGAGTAAACGATCCGACAGTTCTGTATTCTCACTTATAGATTCACTAATACCGAG 180

QY 181 TATGAGTTAGGTATGAAGACCAATTGCACTAGAAAATGATTCATATTCATTTACTTAT 240
DB 181 TATGAGTTAGGTATGAAGACCAATTGCACTAGAAAATGATTCATATTCATTTACTTAT 240

QY 241 CATGATGACCTACCGAGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 300

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QY 841 TTATTAGAAATCGTTGATTTA 861  
 Db 841 TTATTAGAAATCGTTGATTTA 861

# RESULT 7

US-09-815-242-4184  
 ; Sequence 4184, Application US/09815242  
 ; Patent No. US20020061569A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Karl L.  
 ; APPLICANT: Zyskind, Judith W.  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John D.  
 ; APPLICANT: Carr, Grant J.  
 ; APPLICANT: Yamamoto, Robert T.  
 ; APPLICANT: Xu, H. Howard  
 ; TITLE OF INVENTION: Identification of Essential Genes in  
 ; FILE REFERENCE: ELITRA.011A  
 ; CURRENT FILING DATE: 2001-03-21  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 14110  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 4184  
 ; LENGTH: 864  
 ; TYPE: DNA  
 ; ORGANISM: Staphylococcus aureus  
 ; US-09-815-242-4184

Query Match 96.6%; Score 831.6; DB 9; Length 864;  
 Best Local Similarity 98.9%; Pred. No. 4.2e-171;  
 Matches 837; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 ATGAATAAATTAATAGATGAAGTCAATATATGATGCGTGGATGAATAAATCAATCA 75  
 Db 1 ATGAATAAATTAATAGATGAAGTCAATATATGATGCGTGGATGAATAAATCAATCA 60  
 QY 76 ATGAATACTACGCTAGAAAGAAATGTTGTTATTCATTAATGCTGAGGTAACCGCATC 135  
 Db 61 ATGAATACTACGCTAGAAAGAAATGTTGTTATTCATTAATGCTGAGGTAACCGCATC 120  
 QY 136 CGACCAAGTCTGTTATTAATCACTTTAGATCACTAATACCGAGTATGAGTTAGGATG 195  
 Db 121 CGACCAAGTCTGTTATTAATCACTTTAGATCACTAATACCGAGTATGAGTTAGGATG 180  
 QY 196 AAGAGCGCAATGCACTAGAAATGATTCATATCATATTCATCTTATTCATGATGACCTACCA 255  
 Db 181 AAGAGCGCAATGCACTAGAAATGATTCATATCATATTCATCTTATTCATGATGACCTACCA 240  
 QY 256 GCGATGATTAATGATGATTAATGACGAGGAAATTAACAATCTAATAGTAATGAGTGA 315  
 Db 241 GCGATGATTAATGATGATTAATGACGAGGAAATTAACAATCTAATAGTAATGAGTGA 300  
 QY 316 TGAATGCGATATTAAGCAGGTGATGCTTATTAATCAATGAAGCATTTGATTTCAAGT 375  
 Db 301 TGAATGCGATATTAAGCAGGTGATGCTTATTAATCAATGAAGCATTTGATTTCAAGT 360

QY 376 GATGATAGATTAACTGATGAGTAATAAATTAAGTCTACAAAGGCTGCAATAGCAAGT 435  
 Db 361 GATGATAGATTAACTGATGAGTAATAAATTAAGTCTACAAAGGCTGCAATAGCAAGT 420  
 QY 436 GGTCAATGTTGAATGTCGCGCGGTCAAAATGTTAATATGCAAGCGCAAGCCAAATTT 495  
 Db 421 GGTCAATGTTGAATGTCGCGCGGTCAAAATGTTAATATGCAAGCGCAAGCCAAATTT 480  
 QY 496 GATCTTGAACCTTTGGAATGATACACAAACCAAAACAGAGCATTTAATCTTTGCG 555  
 Db 481 GATCTTGAACCTTTGGAATGATACACAAACCAAAACAGAGCATTTAATCTTTGCG 540  
 QY 556 GTTATGAGTGCAGCAGATATGCTTAATGTCATGATACATCAATTAAGAACTTTGAAAGT 615  
 Db 541 GTTATGAGTGCAGCAGATATGCTTAATGTCATGATACATCAATTAAGAACTTTGAAAGT 600  
 QY 616 TATAGTTATCAATTAAGTATGATGATGTCAGATTAAGTGAATTTATGACTGATGCT 675  
 Db 601 TATAGTTATCAATTAAGTATGATGATGTCAGATTAAGTGAATTTATGACTGATGCT 660  
 QY 676 GATGAAGCAAAATTAAGTAAAGTGGCAGCGCATCTTGAAATTAATTAAGTACGTAAC 735  
 Db 661 GATGAAGCAAAATTAAGTAAAGTGGCAGCGCATCTTGAAATTAATTAAGTACGTAAC 720  
 QY 736 GTGAGTTATTAAGGAAAGATGCGCAGAAAGTAAATTAATGATTTATCATAGAGCGAGCA 795  
 Db 721 GTGAGTTATTAAGGAAAGATGCGCAGAAAGTAAATTAATGATTTATCATAGAGCGAGCA 780  
 QY 796 GTGATGAGTAATCAACCAATTAATGATGATCAATCAATCAATCAATCAATCAATCAAT 855  
 Db 781 GTGATGAGTAATCAACCAATTAATGATGATCAATCAATCAATCAATCAATCAATCAAT 840  
 QY 856 GATTTA 861  
 Db 841 GATTTA 846

## RESULT 8

US-10-282-122A-34531  
 ; Sequence 34531, Application US/10282122A  
 ; Publication No. US20040029129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Karl  
 ; APPLICANT: Zyskind, Judith  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Forsyth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 ; FILE REFERENCE: ELITRA.034A  
 ; CURRENT FILING DATE: 2003-02-20  
 ; PRIOR FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931

Query Match	52.2%;	Score 449.8;	DB 13;	Length 879;
Best Local Similarity	70.2%;	Pred. No. 5.1e-88;		
Matches 604; Conservative	0;	Mismatches 257;	Indels 0;	Gaps 0;

Qy	1	ATACCAATCTCCCGATGAATTAATTAATTAATGAAGCAATATGAATATCGGTGG	60
Ds	1	ATGAAGAACTCAAGTGAATTAATTAATTAATTAATCACTCACTGAAATGAATGA	60
Qy	61	ATTAATTAATTCAGTAATGAGATCTCAGCTAGAAGAAAGTATGTTGATTCATTTAAATGCT	120
Ds	61	ATTCATATCATCCCATTTAAAACTATTTAGAGAAAGATGAAATTTTCATTAATGCT	120
Qy	121	GGAGGTAAACGATCCGACCACTTCTGTTATTACTCACTTAGATTCACTAAATACCGAG	180
Ds	121	GGTGTAAAGATCGACCACTCATATTAATTAATCACTAAAAATGCTTAAACAAAGT	180
Qy	181	TATAGTTAGTATGATGAAGACGCAATTCACCTAAGAAATGATCATATTCATTCATT	240
Ds	181	TATCAACAAGACTAAATATGTCCTTAGACATGGAATATGATCTACTTATTCCTTAAT	240
Qy	241	CATGATGACCTTACCGCATGATATATGATATTTATGACGAGAAATTAACAAATCT	300
Ds	241	CATGATGATTTCCACGCAATGATATATACATTTACCGTGAAGAAATTAACAAATCAT	300
Qy	301	AAAGTATATGAGAGTGGACCTGCAATTATACAGCTATTCCTTATTAATCAAGATTT	360
Ds	301	AAAGTTATATGAGATGGAAAGCCATTTCTGCTGATGATATTTAACAAAGCTTT	360
Qy	361	GAACTTATTTCAAGTATGATAGATTAACGTGATGAATTAATAAAAGTTCTACACCG	420
Ds	361	GAATTAGTTTCAATGATACATACATTTGAAATATGATGAAATTAAGTATTTATTAAGA	420
Qy	421	CTGTCAATAGCAAGTGTCTCATGTTGAAATGTCGCGCGTCAAAATGTTAATGCAAGC	480
Ds	421	CTTTCAAAAGCAAGTGCACATTTGGGATGCTGGTGGCCAAACGCTTGATGGAAGT	480
Qy	481	GAAAGCCAAACAATGATCTTGAAACTTGGAAATGATACAAACCAAAAACAGAGAG	540
Ds	481	GAAAGCAATCATTTCTGTTTGAATCTTTAGAACTTTATATGAATCTAAGACAGCGCT	540
Qy	541	TATTAACCTTTGCGGTATAGATGACAGACATATCGTATATGATGATCAACTAA	600
Ds	541	TATCAATAATTTTCAGTTATGCGCTGCGGTACACTGCTCAATTAAGCAAAATATGCT	600
Qy	601	GAACTTTAGAAAGTTATAGTATATCATTTAGATATGATGTTCCAGATTAAGATGATTA	660
Ds	601	AAGAAATTTAGATGAATTTAGTCATCATTTAGAGATGATGTTCAAAATTAAGATGATTA	660
Qy	661	TTAGACTGCTATGATGATGAAGCAAAAGTTAGTATTAATAAATGGGACGACATCTGAAT	720
Ds	661	CTGAGATGTTATGATGATGAATCAAACTTGGCAAAAATGAGCGATGATATAGTAAT	720
Qy	721	AAATAAAGTACGTACGTAGTTTATAGGAAGATGGCCAGAAATTAATTTGACTTAT	780
Ds	721	CATAAAGTACTATGTTCTTTACTTGGAAAGAAAGACAGAGAAAGTTAAACAAT	780
Qy	781	CATAGAGCGCAGCACTGATGAATCAACGAAATGATAGACATTCATATCAAAACAC	840
Ds	781	CATCATATCTTGCTATGACATGCTTAATCAAAATTTCTGATCAATATGATCTTCTGAA	840

RESULT 9  
US-10-282-122A-35068

```

PUBLICATiON NO.: US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITFA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35068
LENGTH: 879
TYPES: DNA
ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-35068

```

Query Match	51.6%;	Score 444.2;	DB 13;	Length 879;
Best Local Similarity	-69.9%;	Pred. No. 8.4e-87;		
Matches 599;	Conservative 0;	Mismatches 258;	Indels 0;	Gaps 0;

Qy	1	ATATGCAATCTCCCATGAAATTAATTAATAGTAGAAGCAATTAATGAAATTAATCGATTGCG	60
	2	ATATGCAATCTCCCATGAAATTAATTAATAGTAGAAGCAATTAATGAAATTAATCGATTGCG	60
	3	ATATGCAATCTCCCATGAAATTAATTAATAGTAGAAGCAATTAATGAAATTAATCGATTGCG	60
Db	1	ATGCGCAAAAGAAATCAATGATGAATTAATTAATCAAAATTAATAGCGCTTGAGCGGTGA	60
Qy	61	ATTAAATTAATTCAGTATGATCTCTACGTAGAAAGAAAGTATGTTGTAATCAATTAAAGCT	120
Db	61	ATCGAAACTTCACCACTAAATATCGAATTTAGAGAAAGTATGCAATATCTCTCAATGCG	120
Qy	121	GGAGGTAAACGCATCCGACCAAGTTCTGTATTACTCACTTAGATTCACTAAATATCCGAG	180
Db	121	GGGGGTAAAGAAATTAAGACCACTTCTGTATATTTTAAACATTAGATGTAATTAATCAAGAT	180
Qy	181	TATGATTAGTATAGAGCGCAATTCACCTAGAAATGATTCATACATATTCACCTATT	240

Page 8

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/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,655
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,991
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 2892
/ LENGTH: 413
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-09-815-242-2822

Query Match      48.0%; Score 413; DB 9; Length 413;
Best Local Similarity 100.0%; P-adj. No. 3.8e-80;
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 160 TTAAATTCATTAATACCGAGTATGAGTTAGATGATGAAAGCCGCAATTGCCTAGAAATG 219
DB 413 TTAAATTCATTAATACCGAGTATGAGTTAGATGATGAAAGCCGCAATTGCCTAGAAATG 354
OY 220 ATTGATACATATTCACCTTATTCATGATGACCTCAACGAGTATGATGATGATATATGCA 279
DB 353 ATTGATACATATTCACCTTATTCATGATGACCTCAACGAGTATGATGATGATATATGCA 294
OY 280 CGAGGAAATTTAACAAATCATTAAGATATGATGATGATGATGATGATGATGATGAT 339
DB 293 CGAGGAAATTTAACAAATCATTAAGATATGATGATGATGATGATGATGATGATGAT 234
OY 340 GCTTATTAATCAATGAAGCATTTGAACCTATTCAGATGATGATGATGATGATGATGATGAT 399
DB 233 GCTTATTAATCAATGAAGCATTTGAACCTATTCAGATGATGATGATGATGATGATGAT 174
OY 400 AAAATTAAGTTCTTACACGCGCTGTCAATAGCAAGTGTCAATGTTGCAATGCTGCGCGGT 459
DB 173 AAAATTAAGTTCTTACACGCGCTGTCAATAGCAAGTGTCAATGTTGCAATGCTGCGCGGT 114
OY 460 CAAATGTTAGTATGCAAAAGGAGGCAACCAATTTGATCTTTGAAACCTTTGAAATGATA 519
DB 113 CAAATGTTAGTATGCAAAAGGAGGCAACCAATTTGATCTTTGAAACCTTTGAAATGATA 54
OY 520 CACAAAACAAAACAGAGGCAATTATTAATCTTTGGCTTATGATGATGACGACGAGA 572
DB 53 CACAAAACAAAACAGAGGCAATTATTAATCTTTGGCTTATGATGATGACGACGAGA 1

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Query Match	29.3%	Score 252.6;	DB 13;	Length 882;
Best Local Similarity	59.3%;	Freq. No. 4.2e-45;		
Matches 493;	Conservative 0;	Mismatches 294;	Indels 0;	Gaps 0
61	ATAAATAACAGTATGATGATCTCAAGTGAAGAAAGTGTGTGATTCATTAAATGCT			120
67	ATMAAGACGAATATGCAACTAGACTAAAGATCCATGTTATTTCTATTCACAGA			126
121	GGAGGTAAACGATCCGACAGCTCTGTATATCTCCTTAATTCACATTAACCGAG			180
127	GGGGGAAACGGATTCGTCATGCTATGTTTCGTCAGCTTCAGCTTTAAAGTAAAT			186
181	TATGATTTAGTATGATGAGAGCGCAATTGCACTAGAAATGATCATATTCATTATT			240
187	CCGCTTTTAGTGTAAACCGCAACGCGTTAGAAATGATTCACATCCAGCTTATT			246
241	CATGATGACCTTCCAGCGATGATTAATGATTAATGATGAAGAGAAATTAACAAATCAT			300
247	CATGATGATCTACCGACATGATATGATATGATGATGATGATGATGATGATGATGAT			306
301	AAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT			360
307	AAAGTTTGGGATGACACTGCGATTTTGGCAGAAATGCTTTTACACGCTCGCTTTT			366
361	GAACTTATTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT			420
367	TCTATTTTAGTGAAGACGATATTTATCTTTTGAAGACGCAATGCTTTGATTAACAA			426
421	CTGTCAATAGCAAGTGTGATGTTGGAATGTTGCGCGGTCAAAATGTTAGATGACAAAC			480
427	ATTAGTTTATGAGCGGTGACAGAAAGAAATGTTGTGTGTCAACTTGGCAGCTTGGAGCG			486
481	GAAGGCAACCAATTGATCTTGAATCTTGAATGATGATGATGATGATGATGATGATGAT			540
487	GAATAACCAACGATGACGCTGAAAGATTTATCATCCATTCATGACGAAATTAAGGATGA			546





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 15:49:03 ; Search time 23 Seconds  
(without alignments)  
644.202 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 287  
Sequence: 1 MTNHPMKLIDENVNLSVA.....ELTGIDQFNTKHLLEIVDL 287

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents, AA:\*  
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3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCITUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfltest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	35.5	293	3	US-09-276-873-2
2	37	12.9	302	4	US-09-134-001C-3171
3	17	5.9	280	4	US-09-634-238-303
4	17	5.9	312	4	US-09-107-532A-6724
5	15	5.2	297	4	US-09-934-903-14
6	15	5.2	307	4	US-09-543-681A-5908
7	14	4.9	297	1	US-08-534-910B-7
8	14	4.9	297	1	US-08-534-910B-8
9	14	4.9	297	1	US-08-534-910B-10
10	14	4.9	297	3	US-08-886-466-2
11	14	4.9	297	3	US-09-475-304-2
12	14	4.9	297	4	US-09-101-126-3
13	14	4.9	297	4	US-09-367-528A-5
14	11	3.8	291	3	US-09-275-742-2
15	9	3.1	320	3	US-09-217-609A-6
16	9	3.1	320	3	US-08-873-235B-6
17	9	3.1	342	4	US-09-540-225-2512
18	9	2.8	219	4	US-09-328-352-5590
19	8	2.8	226	4	US-09-148-545-145
20	8	2.8	285	3	US-09-187-050-12
21	8	2.8	293	2	US-08-284-465-4
22	8	2.8	294	2	US-08-284-465-3
23	8	2.8	294	2	US-08-284-465-8
24	8	2.8	297	1	US-08-534-910B-6
25	8	2.8	297	1	US-08-534-910B-9
26	8	2.8	297	4	US-09-367-528A-1
27	8	2.8	297	4	US-09-367-528A-3

28	8	2.8	299	4	US-09-489-039A-12733	Sequence 12733, A
29	8	2.8	393	3	US-09-187-050-2	Sequence 2, Appl1
30	8	2.8	393	3	US-09-187-050-14	Sequence 14, Appl1
31	8	2.8	393	3	US-09-187-050-16	Sequence 16, Appl1
32	8	2.8	393	3	US-09-187-050-18	Sequence 18, Appl1
33	8	2.8	393	3	US-09-187-050-20	Sequence 20, Appl1
34	8	2.8	393	3	US-09-187-050-22	Sequence 22, Appl1
35	8	2.8	393	3	US-09-187-050-24	Sequence 24, Appl1
36	8	2.8	393	3	US-09-187-050-26	Sequence 26, Appl1
37	8	2.8	393	3	US-09-187-050-27	Sequence 27, Appl1
38	8	2.8	393	3	US-09-187-050-28	Sequence 28, Appl1
39	8	2.8	393	3	US-09-187-050-29	Sequence 29, Appl1
40	8	2.8	393	3	US-09-187-050-30	Sequence 30, Appl1
41	8	2.8	393	3	US-09-187-050-31	Sequence 31, Appl1
42	8	2.8	393	3	US-09-187-050-32	Sequence 32, Appl1
43	8	2.8	393	3	US-09-187-050-33	Sequence 33, Appl1
44	8	2.8	393	3	US-09-187-050-34	Sequence 34, Appl1
45	8	2.8	401	4	US-09-252-991A-26387	Sequence 26387, A

ALIGNMENTS

RESULT 1  
US-09-276-873-2  
; Sequence 2, Application US/09276873  
; Patent No. 6107058  
; GENERAL INFORMATION:  
; APPLICANT: Wilding, Edwina Imogen  
; APPLICANT: Gwynn, Michael  
; TITLE OF INVENTION: 1SPA  
; FILE REFERENCE: GM10208  
; CURRENT APPLICATION NUMBER: US/09/276, 873  
; CURRENT FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-276-873-2

Query Match 35.5%; Score 102; DB 3; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	96	KLTHKRYGEMTALILAGDALLTKAFELISSDRLTDEVKIKYQLRLSIASGHVGVGGQM	155
DB	96	KLTHKRYGEMTALILAGDALLTKAFELISSDRLTDEVKIKYQLRLSIASGHVGVGGQM	155
QY	156	LDWQSEGPIDLTETEMIKTKTGALLTPVWSAADIANVDD	197
DB	156	LDWQSEGPIDLTETEMIKTKTGALLTPVWSAADIANVDD	197

RESULT 2  
US-09-134-001C-3171  
; Sequence 3171, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134, 001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3171  
; LENGTH: 302

TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3171

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.9e-28;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 ALEMHTYSLIHDDLPMNDYRKGKLTNKKYGEW 106  
DB 79 ALEMHTYSLIHDDLPMNDYRKGKLTNKKYGEW 115

RESULT 3  
US-09-634-238-303  
Sequence 303, Application US/09634238  
Patent No. 6544772  
GENERAL INFORMATION:  
APPLICANT: Glenn, Matthew  
APPLICANT: Hayukkala, Ilkka J.  
APPLICANT: Bloksberg, Leonard, N.  
APPLICANT: Lubbers, Mark W.  
APPLICANT: Dekker, James  
APPLICANT: Christenson, Anna C.  
APPLICANT: Holland, Rose  
APPLICANT: O'Toole, Paul W.  
APPLICANT: Reid, Julian R.  
APPLICANT: Coolbear, Timothy  
TITLE OF INVENTION: Polynucleotides, materials incorporating  
FILE REFERENCE: 11000.104301  
CURRENT APPLICATION NUMBER: US/09/634,238  
CURRENT FILING DATE: 2000-08-08  
NUMBER OF SEQ ID NOS: 422  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 303  
LENGTH: 280  
TYPE: PRT  
ORGANISM: Lactobacillus rhamnosus  
US-09-634-238-303

Query Match  
Best Local Similarity 5.9%; Score 17; DB 4; Length 280;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHDDLPMNDND 91  
DB 70 HTYSLIHDDLPMNDND 86

RESULT 4  
US-09-107-532A-6724  
Sequence 6724, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSER: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 6724:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...312  
SEQUENCE DESCRIPTION: SEQ ID NO: 6724:  
US-09-107-532A-6724

Query Match  
Best Local Similarity 5.9%; Score 17; DB 4; Length 312;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHDDLPMNDND 91  
DB 93 HTYSLIHDDLPMNDND 109

RESULT 5  
US-09-934-903-14  
Sequence 14, Application US/09934903  
Patent No. 6660507  
GENERAL INFORMATION:  
APPLICANT: Koffas, Matthews  
APPLICANT: Odom, J. Martin  
APPLICANT: Schenzle, Andreas J.  
APPLICANT: No. 6660507on, Kelley C.  
APPLICANT: Tomb, Jean-Francois  
APPLICANT: Rouviere, Pierre  
APPLICANT: Picataggio, Stephen  
APPLICANT: Cheng, Qiong  
TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production  
FILE REFERENCE: C11646 US NA  
CURRENT APPLICATION NUMBER: US/09/934,903  
CURRENT FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/229,907  
PRIOR FILING DATE: September 1, 2001  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 14  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Methylobionas 16a  
FEATURE:  
OTHER INFORMATION: Amino acid sequences encoded by ORF7  
US-09-934-903-14

Query Match  
Best Local Similarity 5.2%; Score 15; DB 4; Length 297;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 YSLIHDDLPMNDND 91  
DB 80 YSLIHDDLPMNDND 94

RESULT 6  
US-09-543-681A-5908  
Sequence 5908, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 5908  
LENGTH: 307  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-5908

Query Match 5.2%; Score 15; DB 4; Length 307;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 YSLIHDDLPAMDND 91  
Db 87 YSLIHDDLPAMDND 101

RESULT 7  
US-08-534-910B-7  
Sequence 7, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOYAMA, Tanetoshi  
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding Ther  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-7

Query Match 4.9%; Score 14; DB 1; Length 297;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 EMIHTYSLIHDDLP 85  
Db 76 EMIHTYSLIHDDLP 89

RESULT 8  
US-08-534-910B-8  
Sequence 8, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOYAMA, Tanetoshi  
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding The  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-8

Query Match 4.9%; Score 14; DB 1; Length 297;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 EMHTYSLIHDDLP 85  
DB 76 EMHTYSLIHDDLP 89

## RESULT 9

US-08-534-910B-10  
Sequence 10, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyocho  
APPLICANT: KOYAMA, Tanetsoshi  
TITLE OF INVENTION: Mutated Farnesylphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranylphosphate And Gene Coding Ther  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-10  
Query Match 4.9%; Score 14; DB 1; Length 297;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 72 EMHTYSLIHDDLP 85  
DB 76 EMHTYSLIHDDLP 89

## RESULT 10

US-08-886-466-2  
Sequence 2, Application US/08886466C  
Patent No. 6040165  
GENERAL INFORMATION:  
APPLICANT: Narita, Keishi  
APPLICANT: Ishida, Chika  
APPLICANT: Takeuchi, Yoshie

APPLICANT: Ohto, Chikara  
APPLICANT: Ohnuma, Shinichi  
APPLICANT: Nishino, Tokuzo  
TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE  
FILE REFERENCE: 77670/494  
CURRENT APPLICATION NUMBER: US/09/886,466C  
CURRENT FILING DATE: 1997-07-10  
EARLIER APPLICATION NUMBER: JP 8-191635  
EARLIER FILING DATE: 1996-07-03  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Bacillus stearothermophilus  
US-08-886-466-2

Query Match 4.9%; Score 14; DB 3; Length 297;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 EMHTYSLIHDDLP 85  
DB 76 EMHTYSLIHDDLP 89

## RESULT 11

US-09-475-304-2  
Sequence 2, Application US/09475304  
Patent No. 6225096  
GENERAL INFORMATION:  
APPLICANT: Narita, Keishi  
APPLICANT: Ishida, Chika  
APPLICANT: Takeuchi, Yoshie  
APPLICANT: Ohto, Chikara  
APPLICANT: Ohnuma, Shinichi  
APPLICANT: Nishino, Tokuzo  
TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE  
FILE REFERENCE: 77670/494  
CURRENT APPLICATION NUMBER: US/09/475,304  
CURRENT FILING DATE: 1999-12-30  
EARLIER APPLICATION NUMBER: JP 8-191635  
EARLIER FILING DATE: 1996-07-03  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Bacillus stearothermophilus  
US-09-475-304-2

Query Match 4.9%; Score 14; DB 3; Length 297;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 EMHTYSLIHDDLP 85  
DB 76 EMHTYSLIHDDLP 89

## RESULT 12

US-09-101-126-3  
Sequence 3, Application US/09101126  
Patent No. 6316216  
GENERAL INFORMATION:  
APPLICANT: OHTO, CHIKARA  
APPLICANT: NAKANE, HIROYUKI  
APPLICANT: NISHINO, TOKUZO  
APPLICANT: OHNUMA, SHINICHI  
APPLICANT: HIROOKA, KAZUTAKE  
TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES  
FILE REFERENCE: 77670/566  
CURRENT APPLICATION NUMBER: US/09/101,126

CURRENT FILING DATE: 1999-04-27  
; EARLIER APPLICATION NUMBER: PCT/JP97/03921  
; EARLIER FILING DATE: 1997-10-29  
; EARLIER APPLICATION NUMBER: JP 8-307506  
; EARLIER FILING DATE: 1996-11-05  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 3  
; LENGTH: 297  
; TYPE: PRT  
; ORGANISM: Bacillus stearothermophilus  
; FEATURE:  
; OTHER INFORMATION: 86-92 is an Asp-rich domain  
US-09-101-126-3

Query Match 4.9%; Score 14; DB 4; Length 297;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDL 85  
|||  
Db 76 EMHTYSLIHDDL 89

RESULT 13  
US-09-367-528A-5  
; Sequence 5, Application US/09367528A  
; Patent No. 6395525  
; GENERAL INFORMATION:  
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA  
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene  
; FILE REFERENCE: PR-586  
; CURRENT APPLICATION NUMBER: US/09/367,528A  
; CURRENT FILING DATE: 1999-08-16  
; PRIOR APPLICATION NUMBER: JP97/346686  
; PRIOR FILING DATE: 1997-12-16  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 5  
; LENGTH: 297  
; TYPE: PRT  
; ORGANISM: Bacillus stearothermophilus  
US-09-367-528A-5

Query Match 4.9%; Score 14; DB 4; Length 297;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDL 85  
|||  
Db 76 EMHTYSLIHDDL 89

RESULT 14  
US-09-275-742-2  
; Sequence 2, Application US/09275742  
; Patent No. 6130069  
; GENERAL INFORMATION:  
; APPLICANT: Wilding, Edwin Imogen  
; APPLICANT: Gwynn, Michael  
; TITLE OF INVENTION: 18PA  
; FILE REFERENCE: GMI0205  
; CURRENT APPLICATION NUMBER: US/09/275,742  
; CURRENT FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 2  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-275-742-2

Query Match 3.8%; Score 11; DB 3; Length 291;

Best Local Similarity 100.0%; Pred. No. 0.0087;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 SLIHDDLPMAD 88  
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Db 76 SLIHDDLPMAD 86

RESULT 15  
US-09-217-609A-6  
; Sequence 6, Application US/09217609A  
; Patent No. 6071733  
; GENERAL INFORMATION:  
; APPLICANT: MURAMATSU, Masayoshi  
; APPLICANT: KOIKE, Ayumi  
; APPLICANT: OGURA, Kyozo  
; APPLICANT: KOYAMA, Tanetsoshi  
; APPLICANT: SHIMIZU, Naoto  
; APPLICANT: CHO, Yew-Jin  
; TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenyon & Kenyon  
; STREET: 1025 Connecticut Avenue, NW - Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
; SOFTWARE: WordPerfect 6.1 for Windows  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/217,609A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/873,235  
; FILING DATE: 11-Jun-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TOFFENETTI, Judith L.  
; REGISTRATION NUMBER: 39,048  
; REFERENCE/DOCKET NUMBER: 10235/1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-429-1776  
; TELEFAX: 202-429-0796  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 320 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-217-609A-6

Query Match 3.1%; Score 9; DB 3; Length 320;  
Best Local Similarity 100.0%; Pred. No. 0.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 AGGKRIRPV 48  
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Db 42 AGGKRIRPV 50

Search completed: April 19, 2004, 15:54:52  
Job time : 23 secs

Tue Apr 20 12:43:39 2004

us-09-925-637-64.rapb

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 15:53:23 ; Search time 47 Seconds  
(without alignments)  
1683.366 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 287  
Sequence: 1 MTNLPNNKIDVNNELSVVA.....ELTQIDQFVTKHLEIVDL 287

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Gapop 60.0, Gapext 60.0

Searched: 1124875 seqs, 275673149 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Published Applications AA:\*

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16: /cgn2\_6/ptodata/2/pubppa/US02\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubppa/US01\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppa/US00\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	287	100.0	287	9	US-09-925-637-64
2	287	100.0	287	14	US-10-084-205-64
3	197	68.6	293	9	US-09-815-242-12583
4	192	66.9	288	9	US-09-815-242-5239
5	132	46.0	293	12	US-10-282-122A-44363
6	37	12.9	293	12	US-10-282-122A-70715
7	37	12.9	293	12	US-10-282-122A-71252
8	28	9.8	310	15	US-10-369-493-19922
9	27	9.4	293	12	US-10-282-122A-60940
10	22	7.7	261	15	US-10-369-493-9710
11	20	7.0	284	12	US-10-282-122A-52706
12	18	6.3	295	15	US-10-369-493-18391
13	18	6.3	290	12	US-10-282-122A-74642
14	18	6.3	293	9	US-09-815-242-10630
15	18	6.3	293	12	US-10-282-122A-57289

16	6.3	309	15	US-10-369-493-18752	Sequence 18752, A
17	5.9	265	12	US-10-282-122A-57443	Sequence 57443, A
18	5.9	280	15	US-10-264-213-206	Sequence 206, App
19	5.9	283	15	US-10-264-213-240	Sequence 240, App
20	5.9	306	15	US-10-369-493-10187	Sequence 10187, A
21	5.6	281	12	US-10-282-122A-54639	Sequence 54639, A
22	5.2	287	15	US-10-369-493-19191	Sequence 19191, A
23	5.2	289	12	US-10-282-122A-72262	Sequence 72262, A
24	5.2	294	12	US-10-282-122A-61226	Sequence 61226, A
25	5.2	295	12	US-10-282-122A-53246	Sequence 53246, A
26	5.2	296	15	US-10-369-493-480	Sequence 480, App
27	5.2	296	15	US-10-369-493-21173	Sequence 21173, A
28	5.2	297	9	US-09-934-903-14	Sequence 14, App1
29	5.2	297	9	US-09-934-903-12	Sequence 12, App1
30	5.2	297	10	US-09-941-947A-20	Sequence 20, App1
31	5.2	297	12	US-10-700-003-14	Sequence 14, App1
32	5.2	307	12	US-10-282-122A-68693	Sequence 68693, A
33	4.9	282	15	US-10-369-493-23201	Sequence 23201, A
34	4.9	289	12	US-10-282-122A-51526	Sequence 51526, A
35	4.9	294	15	US-10-369-493-17358	Sequence 17358, A
36	4.9	297	14	US-10-462-698A-76	Sequence 76, App1
37	4.2	153	15	US-10-369-493-16138	Sequence 16138, A
38	4.2	156	15	US-10-369-493-15292	Sequence 15292, A
39	4.2	156	15	US-10-369-493-15657	Sequence 15657, A
40	4.2	294	12	US-10-282-122A-77172	Sequence 77172, A
41	4.2	294	15	US-10-369-493-18010	Sequence 18010, A
42	4.2	295	9	US-09-815-242-11239	Sequence 11239, A
43	4.2	295	12	US-10-282-122A-58515	Sequence 58515, A
44	4.2	295	12	US-10-282-122A-67018	Sequence 67018, A
45	4.2	298	12	US-10-282-122A-73438	Sequence 73438, A

#### ALIGNMENTS

RESULT 1  
US-09-925-637-64  
Sequence 64, Application US/09925637  
Patent No. US2002010338A1  
GENERAL INFORMATION:  
APPLICANT: ChOI  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides  
FILE REFERENCE: PB560  
CURRENT APPLICATION NUMBER: US 09/925,637  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/23773  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US 60/151,933  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: US 08/781,986  
PRIOR FILING DATE: 1997-01-03  
PRIOR APPLICATION NUMBER: US 08/956,171  
PRIOR FILING DATE: 1997-10-20  
PRIOR APPLICATION NUMBER: US 60/009,861  
PRIOR FILING DATE: 1996-01-06  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 64  
LENGTH: 287  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-637-64

Query Match 100.0%; Score 287; DB 9; Length 287;  
Best Local Similarity 100.0%; Pred. No. 5.2e-269;  
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTNLPNNKIDVNNELSVVAIKSVYDTQLEBSMLYSINAGGKRIRPVLLITLDSLNT 60  
DB 1 MTNLPNNKIDVNNELSVVAIKSVYDTQLEBSMLYSINAGGKRIRPVLLITLDSLNT 60  
QY 61 YEIGKSAIATLMTITYSILHDDLPAMNDPDRGKLTNNHKYGGWTAIINGDALTLTAKF 120

Db 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNKKVGEWTAIAGDALITKAF 120  
 QY 121 ELISSDDRLEDEVKIKYLRSLASGHVGVGQMLDMOSEGPIDLETLEMHTKKTGA 180  
 Db 121 ELISSDDRLEDEVKIKYLRSLASGHVGVGQMLDMOSEGPIDLETLEMHTKKTGA 180  
 QY 181 LITFAVMSAADIANVDDTTEKHELESYHGLGMFQIKDDLLDCYGEAKLKKVGSDDLEN 240  
 Db 181 LITFAVMSAADIANVDDTTEKHELESYHGLGMFQIKDDLLDCYGEAKLKKVGSDDLEN 240  
 QY 241 NKSTYVSLGKDGAEKLTYHRDAVDELTOIDEGFNTKLLLEIVDL 287  
 Db 241 NKSTYVSLGKDGAEKLTYHRDAVDELTOIDEGFNTKLLLEIVDL 287

## RESULT 2

US-10-084-205-64  
 / Sequence 64, Application US/10084205  
 / Publication No. US20030049648A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Choi, Gil  
 / TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides  
 / FILE REFERENCE: P515P1  
 / CURRENT APPLICATION NUMBER: US/10/084,205  
 / PRIOR FILING DATE: 2002-02-28  
 / PRIOR APPLICATION NUMBER: PCT/US00/23773  
 / PRIOR FILING DATE: 2000-08-31  
 / PRIOR APPLICATION NUMBER: 60/151,933  
 / NUMBER OF SEQ ID NOS: 74  
 / SOFTWARE: PatentIn Ver. 3.1  
 / SEQ ID NO: 64  
 / LENGTH: 287  
 / TYPE: PRT  
 / ORGANISM: Staphylococcus aureus  
 US-10-084-205-64

Query Match 100.0%; Score 287; DB 14; Length 287;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-269;  
 Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTNLPNNKLIDEVNNELSVAINKSVMDTQLEBSMLYSINAGGKIRPVLILLTDSLNTG 60  
 Db 1 MTNLPNNKLIDEVNNELSVAINKSVMDTQLEBSMLYSINAGGKIRPVLILLTDSLNTG 60  
 QY 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNKKVGEWTAIAGDALITKAF 120  
 Db 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNKKVGEWTAIAGDALITKAF 120  
 QY 121 ELISSDDRLEDEVKIKYLRSLASGHVGVGQMLDMOSEGPIDLETLEMHTKKTGA 180  
 Db 121 ELISSDDRLEDEVKIKYLRSLASGHVGVGQMLDMOSEGPIDLETLEMHTKKTGA 180  
 QY 181 LITFAVMSAADIANVDDTTEKHELESYHGLGMFQIKDDLLDCYGEAKLKKVGSDDLEN 240  
 Db 181 LITFAVMSAADIANVDDTTEKHELESYHGLGMFQIKDDLLDCYGEAKLKKVGSDDLEN 240  
 QY 241 NKSTYVSLGKDGAEKLTYHRDAVDELTOIDEGFNTKLLLEIVDL 287  
 Db 241 NKSTYVSLGKDGAEKLTYHRDAVDELTOIDEGFNTKLLLEIVDL 287

## RESULT 3

US-09-815-242-12583  
 / Sequence 12583, Application US/09815242  
 / Patent No. US20020061569A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Haselbeck, Robert  
 / APPLICANT: Ohlsen, Karl L.  
 / APPLICANT: Zyskind, Judith W.  
 / APPLICANT: Wall, Daniel  
 / APPLICANT: Trawick, John D.  
 / APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.  
 APPLICANT: Xu, H. Howard  
 TITLE OF INVENTION: Identification of Essential Genes in  
 TITLE OF INVENTION: Prokaryotes  
 FILE REFERENCE: ELITRA.011A  
 / CURRENT APPLICATION NUMBER: US/09/815,242  
 / PRIOR FILING DATE: 2001-03-21  
 / PRIOR APPLICATION NUMBER: 60/191,078  
 / PRIOR FILING DATE: 2000-03-21  
 / PRIOR APPLICATION NUMBER: 60/206,848  
 / PRIOR FILING DATE: 2000-05-23  
 / PRIOR APPLICATION NUMBER: 60/207,727  
 / PRIOR FILING DATE: 2000-05-26  
 / PRIOR APPLICATION NUMBER: 60/242,578  
 / PRIOR FILING DATE: 2000-10-23  
 / PRIOR APPLICATION NUMBER: 60/253,625  
 / PRIOR FILING DATE: 2000-11-27  
 / PRIOR APPLICATION NUMBER: 60/257,931  
 / PRIOR FILING DATE: 2000-12-22  
 / PRIOR APPLICATION NUMBER: 60/269,308  
 / PRIOR FILING DATE: 2001-02-16  
 / NUMBER OF SEQ ID NOS: 14110  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO: 12583  
 / LENGTH: 293  
 / TYPE: PRT  
 / ORGANISM: Staphylococcus aureus  
 US-09-815-242-12583

Query Match 68.6%; Score 197; DB 9; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-182;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTNLPNNKLIDEVNNELSVAINKSVMDTQLEBSMLYSINAGGKIRPVLILLTDSLNTG 60  
 Db 1 MTNLPNNKLIDEVNNELSVAINKSVMDTQLEBSMLYSINAGGKIRPVLILLTDSLNTG 60  
 QY 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNKKVGEWTAIAGDALITKAF 120  
 Db 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNKKVGEWTAIAGDALITKAF 120  
 QY 121 ELISSDDRLEDEVKIKYLRSLASGHVGVGQMLDMOSEGPIDLETLEMHTKKTGA 180  
 Db 121 ELISSDDRLEDEVKIKYLRSLASGHVGVGQMLDMOSEGPIDLETLEMHTKKTGA 180  
 QY 181 LITFAVMSAADIANVDD 197  
 Db 181 LITFAVMSAADIANVDD 197

## RESULT 4

US-09-815-242-5239  
 / Sequence 5239, Application US/09815242  
 / Patent No. US20020061569A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Haselbeck, Robert  
 / APPLICANT: Ohlsen, Karl L.  
 / APPLICANT: Zyskind, Judith W.  
 / APPLICANT: Wall, Daniel  
 / APPLICANT: Trawick, John D.  
 / APPLICANT: Carr, Grant J.  
 / APPLICANT: Yamamoto, Robert T.  
 / APPLICANT: Xu, H. Howard  
 TITLE OF INVENTION: Identification of Essential Genes in  
 TITLE OF INVENTION: Prokaryotes  
 FILE REFERENCE: ELITRA.011A  
 / CURRENT APPLICATION NUMBER: US/09/815,242  
 / PRIOR FILING DATE: 2001-03-21  
 / PRIOR APPLICATION NUMBER: 60/191,078  
 / PRIOR FILING DATE: 2000-03-21  
 / PRIOR APPLICATION NUMBER: 60/206,848  
 / PRIOR FILING DATE: 2000-05-23  
 / PRIOR APPLICATION NUMBER: 60/207,727



PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 5239  
LENGTH: 288  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-09-815-242-5239

Query Match 66.9%; Score 192; DB 9; Length 288;  
Best Local Similarity 100.0%; Pred. No. 3.9e-177;  
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 NKKLDEVNNEISVAINKSVMDTOLEESMTYSINAGKRIKPVLLLTLSLNTYEELGM 60  
QY 66 KSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNKKYGEWTAILAGDALLTKAFELISS 125  
DB 61 KSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNKKYGEWTAILAGDALLTKAFELISS 120  
QY 126 DDLRLDEVKIKVQLRLSLASGHVGVGGMLDMQSEGPIDLETLEMHKTKGALLTFA 185  
DB 121 DDLRLDEVKIKVQLRLSLASGHVGVGGMLDMQSEGPIDLETLEMHKTKGALLTFA 180  
QY 186 VMSAADIANDVD 197  
DB 181 VMSAADIANDVD 192

RESULT 5  
US-10-282-122A-44363  
Sequence 44363, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 44363  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-10-282-122A-44363

Query Match 46.0%; Score 132; DB 12; Length 293;  
Best Local Similarity 100.0%; Pred. No. 4.3e-119;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 KSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNKKYGEWTAILAGDALLTKAFELISS 125  
DB 66 KSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNKKYGEWTAILAGDALLTKAFELISS 125  
QY 126 DDLRLDEVKIKVQLRLSLASGHVGVGGMLDMQSEGPIDLETLEMHKTKGALLTFA 185  
DB 126 DDLRLDEVKIKVQLRLSLASGHVGVGGMLDMQSEGPIDLETLEMHKTKGALLTFA 185  
QY 186 VMSAADIANDVD 197  
DB 186 VMSAADIANDVD 197

RESULT 6  
US-10-282-122A-70715  
Sequence 70715, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70715
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70715

Query Match          12.9%; Score 37; DB 12; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      70 ALEMHTYSLIHDDLPMANDNDYRGGKLTNNKYYGEM 106
Db      70 ALEMHTYSLIHDDLPMANDNDYRGGKLTNNKYYGEM 106

RESULT 7
US-10-282-122A-71252
; Sequence 71252, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71252
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-71252

Query Match          12.9%; Score 37; DB 12; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      70 ALEMHTYSLIHDDLPMANDNDYRGGKLTNNKYYGEM 106
Db      70 ALEMHTYSLIHDDLPMANDNDYRGGKLTNNKYYGEM 106

RESULT 8
US-10-369-493-19922
; Sequence 19922, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19922
; LENGTH: 310
; TYPE: PRT
; ORGANISM: No. US20030233675A1loc punctiforme
US-10-369-493-19922

Query Match          9.8%; Score 28; DB 15; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.7e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 SLIHDDLPMANDNDYRGGKLTNNKYYGE 105
Db      94 SLIHDDLPMANDNDYRGGKLTNNKYYGE 121

RESULT 9
US-10-282-122A-60940
; Sequence 60940, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 60940
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; US-10-282-122A-60940

Query Match
Best Local Similarity 9.4%; Score 27; DB 12; Length 293;
                          100.0%; Pred. No. 1.5e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 ALEMTHTYSLIHDDLPAMDNDYRRGK 96
DB 72 ALEMTHTYSLIHDDLPAMDNDYRRGK 98

RESULT 10
; US-10-369-493-9710
; Sequence 9710, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 9710
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Desulfitobacterium hafnense
; US-10-369-493-9710

Query Match
Best Local Similarity 7.7%; Score 22; DB 15; Length 261;
                          100.0%; Pred. No. 9.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IHTYSLIHDDLPAMDNDYRRG 95
DB 43 IHTYSLIHDDLPAMDNDYRRG 64

RESULT 11
; US-10-282-122A-52706
; Sequence 52706, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Malone, Cheryl
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
```

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; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 52706
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Clostridium botulinum
; US-10-282-122A-52706

Query Match
Best Local Similarity 7.0%; Score 20; DB 12; Length 294;
                          100.0%; Pred. No. 9e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLPAMDND 91
DB 75 EMHTYSLIHDDLPAMDND 94

RESULT 12
; US-10-369-493-18391
; Sequence 18391, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 18391
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Lactococcus lactis
; US-10-369-493-18391

Query Match
Best Local Similarity 6.3%; Score 18; DB 15; Length 285;
                          100.0%; Pred. No. 7.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 SLIHDDLPAMDNDYRRG 95
DB 74 SLIHDDLPAMDNDYRRG 91
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RESULT 13
US-10-282-122A-74642
; Sequence 74642, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 74642
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74642

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Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 SLIHDDLPAMDNDYRGG 95
Db      75 SLIHDDLPAMDNDYRGG 92

RESULT 14
US-09-815-242-10630
; Sequence 10630, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.

```

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; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10630
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10630

Query Match      6.3%; Score 18; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      71 LEMHTYSLIHDDLPAMD 88
Db      71 LEMHTYSLIHDDLPAMD 88

RESULT 15
US-10-282-122A-57289
; Sequence 57289, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931

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Tue Apr 20 12:43:39 2004

us-09-925-637-64.rapb

Page 7

; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 57289  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-10-282-122A-57289

Query Match 6.3%; Score 18; DB 12; Length 293;  
Best Local Similarity 100.0%; Pred. No. 7.7e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 71 LEMHTYSLIHDDLPAMD 88  
|||  
Db 71 LEMHTYSLIHDDLPAMD 88

Search completed: April 19, 2004, 15:59:38  
Job time : 47 secs

Tue Apr 20 12:43:40 2004

us-09-925-637-64.rml

Page 1

GenCore version 5.1.6  
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Run on: April 20, 2004, 08:08:02 ; Search time 64 Seconds  
(without alignments)

2488.608 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 1453

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 segs, 277475446 residues

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Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

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6: /cg2n2\_6/ptodata/2/ina/backfiles1.seg:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1453	100.0	1893	4	US-08-956-171E-155
2	1456	98.8	882	3	US-09-276-873-1
3	1015	69.9	909	4	US-09-134-001C-334
4	657	45.2	894	1	US-08-534-910B-4
5	656	45.1	894	1	US-08-534-910B-5
6	654	45.0	893	1	US-08-534-910B-1
7	653	44.9	894	1	US-08-534-910B-2
8	650	44.7	894	1	US-08-534-910B-3
9	650	44.7	894	1	US-08-886-466-1
10	650	44.7	894	3	US-09-475-304-1
11	650	44.7	894	4	US-09-101-126-4
12	650	44.7	894	4	US-09-367-528A-4

13	645	44.4	894	1	US-08-534-910B-1	Sequence 1, Appl1
14	644	44.3	894	4	US-09-367-528A-2	Sequence 2, Appl1
15	551	37.8	876	3	US-09-275-742-1	Sequence 1, Appl1
16	549	37.8	1001.1	4	US-08-961-527-76	Sequence 76, Appl1
17	533	36.7	939	4	US-09-107-532A-3070	Sequence 3070, Ap
18	530.5	35.8	885	3	US-09-187-050-11	Sequence 11, Appl
19	530.5	35.8	1179	3	US-09-187-050-13	Sequence 13, Appl
20	530.5	35.8	1179	3	US-09-187-050-15	Sequence 15, Appl
21	530.5	35.8	1179	3	US-09-187-050-17	Sequence 17, Appl
22	530.5	35.8	1179	3	US-09-187-050-19	Sequence 19, Appl
23	530.5	35.8	1179	3	US-09-187-050-21	Sequence 21, Appl
24	530.5	35.8	1179	3	US-09-187-050-23	Sequence 23, Appl
25	530.5	35.8	1179	3	US-09-187-050-25	Sequence 25, Appl
26	530.5	35.8	1889	3	US-09-187-050-13	Sequence 1, Appl1
27	536.5	35.5	891	4	US-09-534-903-13	Sequence 13, Appl
28	457.5	34.2	1830121	4	US-09-557-884-1	Sequence 1, Appl1
29	457.5	34.2	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
30	487.5	33.6	96109	4	US-09-596-002-35	Sequence 35, Appl1
31	482	33.2	924	4	US-09-543-681A-1736	Sequence 1736, Ap
32	481	33.1	1029	4	US-09-540-235-692	Sequence 692, Ap
33	480.5	33.1	900	4	US-09-489-039A-5562	Sequence 5562, Ap
34	480	33.0	847	4	US-09-534-238-85	Sequence 85, Appl
35	474.5	32.7	1071	4	US-09-552-991A-10000	Sequence 10000, A
36	474.5	32.7	1206	4	US-09-552-991A-9816	Sequence 9816, Ap
37	474.5	32.7	4515	4	US-09-552-991A-10037	Sequence 10037, A
38	465.5	32.0	1131	4	US-09-420-211-1	Sequence 1, Appl1
39	442	30.4	927	4	US-09-328-352-64	Sequence 64, Appl
40	438.5	30.2	466	3	US-08-573-235B-28	Sequence 28, Appl
41	438.5	30.2	466	3	US-08-573-235B-28	Sequence 28, Appl
42	438	30.1	1087	4	US-09-549-848B-15	Sequence 15, Appl
43	438	30.1	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
44	405	27.9	1914	4	US-09-634-238-41	Sequence 41, Appl
45	376.5	25.9	909	1	US-07-783-705A-7	Sequence 7, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-956-171E-155/c  
Sequence 155, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956, 171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009, 861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781, 986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman



```

Db      481 GAAGGCAACCAATTCATTTGAACTTTGGAAAATGATACAAAACAAAACAGAGACA 540
Qy      181 LeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLys 200
Db      541 TTATTAACTTTGCGGTATGAGTGACAGCATATCGCTAATGATGATGATCACTAAA 600
Qy      201 GIuH1sLeuGluSerTyrSerTyrHisLeuGluYMetMetPheGlnIleLysAspAspLeu 220
Db      601 GAACATTTCGAAAGATTATGATATCATTTAGGTATGATGATTCACATTTAAAGATTTTA 660
Qy      221 LeuAspCysTyrGlyAspGluAlaLysLeuGluYlYsLysValGlySerAspLeuGluAsn 240
Db      661 TTAGACTGCTATGCTGATGATGACCAAGTATGTAATAAAGTGGCAGCGATCTTGAAAT 720
Qy      241 AsnLysSerThrTyrValSerLeuLeuGluYlYsAspGlyAlaGluAspLysLeuThrTyr 260
Db      721 AATTAAGAGTACGTACGTGATGATTTATAGGAAAGATGGCGAGAGATTAATGACTTAT 780
Qy      261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
Db      781 CATAGAGACGACGACGTGATGATGATTAAGCAAAATTGATGAACTTCAATACAAAACAC 840
Qy      281 LeuLeuGluIleValAspLeu 287
Db      841 TTATTAGAAATCGTTGATTTA 861

RESULT 3
US-09-134-001C-334
Sequence 334, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lytn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 334
LENGTH: 909
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-334

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Alignment Scores:
Pred. No.: 1,08e-120 Length: 909
Score: 1015.00 Matches: 197
Percent Similarity: 82.93% Conservative: 41
Best Local Similarity: 68.64% Mismatches: 49
Query Match: 69.86% Indels: 0
Gaps: 0

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US-09-925-637-64 (1-287) x US-09-134-001C-334 (1-909)

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Qy      1 MetThrAsnLeuPheMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
Db      28 ATGAAGAAACTACACATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 87
Qy      21 IleAsnLysSerValMetAspThrGlnLeuGluGluSerMetLeuTyrSerLeuAsnAla 40
Db      88 ATACATCATCTCCCATTAATAAATTAATTAAGAGAAAGTAAAGAAATCTCTTAATAGCT 147
Qy      41 GlyGlyLysArgIleArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGlu 60
Db      148 GGTGTAAAGATACAGCACTGATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 207
Qy      61 TyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIle 80

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Db      208 TATCAACAAGACTAAATTAAGTCTTTAGCATTTGAAATGATTCATACATTAATTTTAAT 267
Qy      81 HisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgLysLysLeuThrAsnHis 100
Db      268 CATGATGATTTACAGCAATGATTAATGATGATTAATGATTAATGATTAATGATTAATGATTA 327
Qy      101 LysValTyrGlyGluThrPheAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120
Db      328 AAGTTTATGTTAAAGAAAGCAAGCATTTGCTGGTGAATGATTAATTAACAAAAGCTTTT 387
Qy      121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg 140
Db      388 GAATGATGTTCTATGATTAATCATACATTAAGATGATTAAGATGATTAATTAATTAAGAA 447
Qy      141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSer 160
Db      448 CTTTCAAAAGCAAGTGAACATTTGGAAATGTGTGGCCAGCCGCTTGATATGAAAGT 507
Qy      161 GIuGlyGlnProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAla 180
Db      508 GAAGGAGATGCATTCGTTTGAATCTTTAGATCAATTCATGAATCAATGAACAGCGCT 567
Qy      181 LeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLys 200
Db      568 TTACTTAATTTTCAGTTATGCTGCTGGCTAGACATTCCTCAATGACAAACAAATATTGCT 627
Qy      201 GIuH1sLeuGluSerTyrSerTyrHisLeuGluYMetMetPheGlnIleLysAspAspLeu 220
Db      628 AAGATTTAGATGATTAATTAATTCATCAATTTTGAATGATGATTTTCAATTAAGATGATTTA 687
Qy      221 LeuAspCysTyrGlyAspGluAlaLysLeuGluYlYsLysValGlySerAspLeuGluAsn 240
Db      688 CTGAGTGTGATGATGATGATGATCAAACTTGCAAAAAGTGGCGATGATATAGTAAAT 747
Qy      241 AsnLysSerThrTyrValSerLeuLeuGluYlYsAspGlyAlaGluAspLysLeuThrTyr 260
Db      748 CATTAAGATCTATATGTTCTTACTTGAAGAAAGAGCGAGAAAGTAAACAT 807
Qy      261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
Db      808 CATCAATATTCGTCATGATGATGATGATCAATTCATCAATTCATCAATTCATGAA 867
Qy      281 LeuLeuGluIleValAspLeu 287
Db      868 TTAGTGAATTTGTTGATTTTA 888

```

```

RESULT 4
US-08-534-910B-4
Sequence 4, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyozo
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding The
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows

```



```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Tofteneft, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-4

Alignment Scores:
Pred. No.: 9.56-75 Length: 894
Score: 657.00 Matches: 133
Percent Similarity: 68.10% Conservative: 57
Best Local Similarity: 47.67% Mismatches: 83
Query Match: 45.22% Indels: 6
Gaps: 2

US-09-925-637-64 (1-287) x US-08-534-910B-4 (1-894)
QY 1 MethrshnleuprometlaenlyleuileaspjlvlaasnaenleuSERVALaia 20
DB 1 ATGCGCGAGCTTTCAGTTGAGACAGTTTCACAGCAAGCAAAACAGCGCGGAAACAGCG 60
QY 21 llaenlysevalmet-----AspThrlneugluclusermetleuYr 36
DB 61 CTCGCCCGTATNAGAGCGCGTTAGAGCGCGCGAGAGCTGAAAAAGCGAGCGGCTNC 120
QY 37 SerleuanaalaglylylyrargileargprovalleuileuileuThrlleuapser 56
DB 121 TCATTGAGAGCGCGCGCAACGATCCGTCGCTGCTTGTGCCACCGCTCGCGCG 180
QY 57 leuathnrgluYrGluGluMetlysevalallealeuGluMetleHstr 76
DB 181 CTCGGCAAAAGACCGCGCGCTCGGATTCGCCGCTCGCGCGATGAATGATCCATAG 240
QY 77 TyrsereuleilehisapleuPleuPleuMetaspaaspaaspaTyraargglylys 96
DB 241 CACTCTTTCATCCATGATGATGATTCGCGAGCATGACACATGATTCGCGCGCGCAAG 300
QY 97 leuathnshlsyvalyYrGluYrThrlaalleuHaglyleaplaaleu 116
DB 301 CCGAGCAACCATTAAGTGTTCGCGAGCGCATGCGCATCTTGGGGGGAGCGGCTGTG 360
QY 117 Thrlyalapehgleuleuileser-----SerAspaaspaThrlaapgluVallys 134
DB 361 ACGTACCGGTTTCATGATGATCCAGAAATGACATGAGCGATCCCTCCGTCGCGCG 420
QY 135 lleyvalleuGluGluSerleleaserclyHlsvalyMetvalyglyYrGln 154
DB 421 CTTCGGCTCATCGACGCGCTGCGAAAGCGCGCTCGGAGAGAGTGTGCGCGGTGAG 480
QY 155 MetleuapmetcginsergluglyGlnProileapleuGluThrlleuGluMetleHs 174
DB 481 GCACCGCATATGAGAGAGAGAGGAGAAACGTCGCTTCGAGCTCGAATCATTCAT 540
QY 175 lyethrlyshrglyalaleuThrlaaleuThrlaaleuThrlaaleuThrlaaleu 194

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DB 541 CGGCTAAACCGGAAAAATCTGCATACAGCGTGCAGCGCGCGCTTCATGCGCGCG 600
QY 195 ValaspaepThrThrlYrGluHlsleuGluSerTyrseryrHlsleuGlyMetlePhe 214
DB 601 GGTATGCCCGGCAACCGCGGAGGCTTGACCAATTCGCCGCCCATCTGAGCGCTGCTT 660
QY 215 GlnllelyaspaaspaPleuPleuPleuPleuPleuPleuPleuPleuPleuPleu 234
DB 661 CAATTCGCGATGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 720
QY 235 GlyseraspaPleuGluasnaenlyseXThrlYrValserleuGluGlyYrAspJlvla 254
DB 721 GCGACGCGACCAAGACCAACCAAGCGACGATTCAGCGCTGCTGCTGCGCGCGCG 780
QY 255 GluaspyrleuThrlYrHlsargaspaalalavalaspyrleuThrlleasp 273
DB 781 AAGAAAAGTTGAGCTTCATATCGAGCGCGCGCGCATTTACGAGACCGGAC 837

RESULT 5
US-08-534-910B-5
Sequence 5, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoza
APPLICANT: KOYAMA, Tanetsoshi
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
TITLE OF INVENTION: OF Synthesizing Geranylgeranyl diphosphate And Gene Coding The
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Kenyon & Kenyon
SERIAL: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Tofteneft, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-5

Alignment Scores:
Pred. No.: 1.286-74 Length: 894
Score: 656.00 Matches: 133

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Percent Similarity: 67.38% Conservative: 55  
 Best Local Similarity: 47.67% Mismatches: 85  
 Query Match: 45.15% Indels: 6  
 DB: 1 Gaps: 2

US-09-925-637-64 (1-287) x US-08-534-910B-5 (1-893)

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QY      1 MetThrAsnLeuPromeTasnLysLeuLeuLeuAspGluValAsnAsnGluLeuSerValAla 20
DB      1 ATGGCGGACGCTTTCAGTGAACAGTTTCTCAACGACAAAAACAGCGCGGTGAAACACGCG 60
QY      21 IleAsnLysSerValMet-----AspThrGlnLeuGluGluSerMetLeuTyr 36
DB      61 CTCCTCCGTTATATAGAGCGCTTAGAAGGCGCGGAAAGCTGAAAAAGCGCATGCGCTAC 120
QY      37 SerLeuAsnAlaGlyGlyArgGlyLeuArgProValLeuLeuLeuLeuLeuLeuLeuAspSer 56
DB      121 TCATTGAGCGCGCGCGGAAACGAATCCGTCGCTGCTCTCTCCACCGCTTACGCGG 180
QY      57 LeuAsnThrGluTyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThr 76
DB      181 CTCGGGAAAGACCGCGCGGTGCGGATTCGCCGCTGCGCGCATGAAATGATCCATACG 240
QY      77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96
DB      241 TACTCTTTGATCCATGATGATTTGCGGACATGACGACATGATGATTCGCGCGCGCAAG 300
QY      97 LeuThrAsnHisLysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeu 116
DB      301 CCGACGACCATTAAGTGTTCGCGGACGAGGAGTGGCCATTTGCGGGGACGCGGTGTTG 360
QY      117 ThrLysAlaPheGluLeuLeuLeuSer-----SerAspAspArgLeuThrAspGluValLys 134
DB      361 ACGTACGCGCTTTCATGATGATCAACGGAATCAACGATGAGCGCATCCCTCCGCTCGCGG 420
QY      135 IleLysValLeuGluArgLeuSerIleAlaSerGlyHisValGlyMetValGlyLysGln 154
DB      421 CTTCGGCTATGCAACGCGCTGCGGAAAGCGCGCGCGGAAAGGATGATGCGCGCTCAG 480
QY      155 MetLeuAspMetGlnSerGluGlyGlnProIleAspLeuGluThrLeuGluMetIleHis 174
DB      481 GCAGCGCATATGAGAGAGAGAGGAAACGCTGACGCTTCGAGCTCGAATACATTCAT 540
QY      175 LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsn 194
DB      541 CGGCATTAACCGGAAATGCTGCAATACAGCGGTGACGCGCGCGCTTATCGCGCGG 600
QY      195 ValAspAspThrThrLysGluLeuGluLeuSerTyrSerTyrHisLeuGlyMetMetPhe 214
DB      601 GGTGATGCCCGGCAACCGCGGAGCTGACGATTCGCGCGCATCTAGGCGCTTGCCCTT 660
QY      215 GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGluAlaLysLeuGlyLysLysVal 234
DB      661 CAATTCGCGATGATATCTCGATTTGAAAGGCGGAGAAATAATCGGCAAGCGCGCTC 720
QY      235 GlySerAspLeuGluAsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAla 254
DB      721 GGCAGCGACCAAGCAACAAAGAGAGGATTCAGAGCTTCGCTGCGCTGCGCGCGG 780
QY      255 GluAspLysLeuThrTyrHisArgAspAlaAlaValAspGluLeuThrGlnIleAsp 273
DB      781 AAGGAAAGTGGCGCTTCATTCAGAGCGCGCGCGCATTTACGAAAGCGCGAC 837

```

```

STREET: 1 Broadway
CITY: New York
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: No. 5786192epd, Windows 3.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/953,424
FILING DATE: 29-SEP-1992
APPLICATION NUMBER: JP 3-253788
FILING DATE: 01-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Greason, Edward W.
REGISTRATION NUMBER: 18,918
REFERENCE/DOCKET NUMBER: 077670/00310
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-5288
TELEFAX: (212) 425-7200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-333-321-1
Alignment Scores:
Pred. No.: 2.3e-74 Length: 893
Score: 654.00 Matches: 133
Percent Similarity: 67.38% Conservative: 55
Best Local Similarity: 47.67% Mismatches: 85
Query Match: 45.01% Indels: 6
DB: 1 Gaps: 2
US-09-925-637-64 (1-287) x US-08-333-321-1 (1-893)
QY      1 MetThrAsnLeuPromeTasnLysLeuLeuLeuAspGluValAsnAsnGluLeuSerValAla 20
DB      1 ATGGCGGACGCTTTCAGTGAACAGTTTCTCAACGACAAAAACAGCGCGGTGAAACACGCG 60
QY      21 IleAsnLysSerValMet-----AspThrGlnLeuGluGluSerMetLeuTyr 36
DB      61 CTCCTCCGTTATATAGAGCGCTTAGAAGGCGCGGAAAGCTGAAAAAGCGCATGCGCTAC 120
QY      37 SerLeuAsnAlaGlyGlyArgGlyLeuArgProValLeuLeuLeuLeuLeuLeuLeuAspSer 56
DB      121 TCATTGAGCGCGCGCGGAAACGAATCCGTCGCTGCTCTCTCCACCGCTTACGCGG 180
QY      57 LeuAsnThrGluTyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThr 76
DB      181 CTCGGGAAAGACCGCGCGGTGCGGATTCGCCGCTGCGCGCATGAAATGATCCATACG 240
QY      77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96
DB      241 TACTCTTTGATCCATGATGATTTGCGGACATGACGACATGATGATTCGCGCGCGCAAG 300
QY      97 LeuThrAsnHisLysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeu 116
DB      301 CCGACGACCATTAAGTGTTCGCGGACGAGGATGGCCATTTGCGGGGACGCGGTGTTG 360
QY      117 ThrLysAlaPheGluLeuLeuLeuSer-----SerAspAspArgLeuThrAspGluValLys 134

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Db      361  ACGTACCGCTTTCATTGATCAACGAAATGACGATGAGCGCATCCCTCTCCGCG 420
QY      135  ILeYValLeuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      421  CTTCGGCTCATGCAACGGCTGCGCAAGCGCGGTCCGGAAGGATGTCGCGCGTCA 480
QY      155  MetLeuAspMetGlnSerGlyGlnProIleAspLeuGlnThrLeuGlnMetIleHis 174
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      481  GCAGCCGATATGAGAGAGAGGAGAAACGCTACGCTTCGAGCTCGAATACATTCAT 540
QY      175  LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAla 194
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      541  CGGATATAAACCGGGAATAATGCTTCATACAGCTGACCGCGCTTATCGCGCGG 600
QY      195  ValAspAspThrThrLysGlyHisLeuGlnSerTyrSerTyrHisLeuGlyMetMetPhe 214
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      601  GCTGATGCCCGGCAACGCGGAGCTTGACGAATTCGCCGCCCATCTAGCGCTTGCCTT 660
QY      215  GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGlnAlaLysLeuGlyLysVal 234
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      661  CAATTCGCGATGATATCTCGATATGAAAGGCGCAAGAAAAATCGCGCAAGCGGTC 720
QY      235  GlySerAspLeuGlnAsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAla 254
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      721  GGCGAGCAACCAACCAACCAACGATTCACAGCTGCTGCTGCTGCTGCGCGCGG 780
QY      255  GluAspLysLeuThrTyrHisArgAspAlaAlaValAspGluLeuThrGlnIleAsp 273
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      781  AAGGAAAGTTGGCGTTCCATATCGAGCGCGCGAGCCCATTTACGGAACGCCGAC 837

RESULT 7
US-08-534-910B-2
; Sequence 2, Application US/08534910B
; Patent No. 5766911
;
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBARA, Shuhei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoze
; APPLICANT: Koyama, Taneoshi
; TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
; TITLE OF INVENTION: Of Synthesizing Geranylgeranyl diphosphate And Gene Coding Ther
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,910B
; FILING DATE: 28-SEPT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenect, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
;
US-08-534-910B-2
Alignment Scores:
Pred. No.: 3,1e-74 Length: 894
Score: 653.00 Matches: 132
Percent Similarity: 67.38% Conservative: 56
Best Local Similarity: 47.31% Mismatches: 85
Query Match: 44.94% Indels: 6
DB: 1 Gaps: 2
US-09-925-637-64 (1-287) x US-08-534-910B-2 (1-894)
QY      1  MetThrAsnLeuProMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1  ATGGCGCAGCTTTCATGTAACAGTTTCTCAACAGCAAAAAACAGCGGTGGAACAAG 60
QY      21  IleAsnLysSerValMet-----AspThrGlnLeuGlnGlnSerMetLeuTyr 36
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61  CTCTCCGCTTATATAGACGCTTAGAAGCGCGCGCAAGGTGAAGAAAGCGATGCGTAC 120
QY      37  SerLeuAsnAlaGlyGlyLysArgIleArgProValLeuLeuLeuThrLeuAspSer 56
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121  TCATTGAGAGCGCGCGCAACGAATCCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY      57  LeuAsnThrGlyTyrGlyLeuGlyMetLysSerAlaIleAlaLeuGlnMetIleHisThr 76
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      181  CTGGCAAAAGCCCGCGCGTGGATGGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY      77  TyrSerLeuIleHisAspAspLeuProIleMetAspAsnAspAspTyrArgArgGlyLys 96
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      241  TACCTCTTGATCCATGATGATTTGCCAGCATGACACAGATGATTCGCGCGCGCAAG 300
QY      97  LeuThrAsnHisLysValTyrGlyIleThrAlaIleLeuAlaGlyAspAlaLeuLeu 116
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      301  CCGACGAACCATTAAGTTCTCGCGAGCGATGGCATCTTGGCGGCGGAGCGGCTTGTG 360
QY      117  ThrLysAlaPheGluLeuIleSer-----SerAspAspGluLeuThrAspGluValLys 134
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      361  ACGTACCGCTTTCATTGATCAACGAAATGACGATGAGCGCATCCCTCTCCGCG 420
QY      135  ILeYValLeuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      421  CTTCGGCTCATGCAACGGCTGCGCAAGCGCGGTCCGGAAGGATGTCGCGCGTCA 480
QY      155  MetLeuAspMetGlnSerGlyGlnProIleAspLeuGlnThrLeuGlnMetIleHis 174
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      481  GCAGCCGATATGAGAGAGAGGAGAAACGCTGACGCTTCGAGCTCGAATACATTCAT 540
QY      175  LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAla 194
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      541  CGGATATAAACCGGGAATAATGCTTCATACAGCTGACCGCGCTTATCGCGCGG 600
QY      195  ValAspAspThrThrLysGlyHisLeuGlnSerTyrSerTyrHisLeuGlyMetMetPhe 214
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      601  GCTGATGCCCGGCAACGCGGAGCTTGACGAATTCGCCGCCCATCTAGCGCTTGCCTT 660
QY      215  GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGlnAlaLysLeuGlyLysVal 234
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      661  CAATTCGCGATGATATCTCGATATGAAAGGCGCAAGAAAAATCGCGCAAGCGGTC 720
QY      235  GlySerAspLeuGlnAsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAla 254
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      721  GGCGAGCAACCAACCAACCAACGATTCACAGCTGCTGCTGCTGCTGCTGCGCGG 780
QY      255  GluAspLysLeuThrTyrHisArgAspAlaAlaValAspGluLeuThrGlnIleAsp 273
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 781 AAGAAAAGTTGGCTTCATATGAGCGCGAGCCGCAATTACGAAAGCCGAC 837

RESULT 8  
US-08-534-910B-3  
Sequence 3, Application US/08534910B  
Patent No. 5766911

GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoze  
APPLICANT: KOYAMA, Tanecoshi  
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding Ther  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 894 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
ORGANISM: *Bacillus stearothermophilus*  
US-08-534-910B-3

Alignment Scores:  
Pred. No.: 7,52e-74 Length: 894  
Score: 650.00 Matches: 132  
Percent Similarity: 67.03% Conservative: 55  
Best Local Similarity: 47.31% Mismatches: 86  
Query Match: 44.74% Indels: 6  
Gaps: 2

US-09-925-637-64 (1-287) x US-08-534-910B-3 (1-894)

QY 1 MetThrasnuLeuBrometAsnuysLeuileAspGluValAsnAsnGluLeuSerValAla 20  
Db 1 ATGGCGAGCTTCAGTTGACAGTTCACACGACAAACAGGCGGTGGAACAGCG 60  
QY 21 IlaAsnuysSerValMet-----AspThrGlnLeuGluGluSerMetLeuTyr 36  
Db 61 CTCTCCGTTATATAGAGCGCTTAGAAGGCGCGGACGCTGAAAAAGCGAGTGGCGTTC 120  
QY 37 SerLeuAsnAlaGlyGlyArgGlyLeuArgProValLeuLeuLeuThrLeuAspSer 56

Db 121 TCATTGAGGCGCGGCGGCAACGAAATCCGTCGCTTCCTGTCACCGCTTCGCG 180  
QY 57 LeuAsnThrGlyTyrGluLeuGlyMetLeuSerAlaLeuAlaLeuGluMetLeuThr 76  
Db 181 CTCGAAAAAGACCCGCGGCGTTCGATTCGCCGTCCGCTCGCGGATTTGAATGATCATAC 240  
QY 77 TyrSerLeuileHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96  
Db 241 TACTCTTGATTCATGATGATGATTTGCCGAGCATGACACATGATTTGCCGCGCGGACG 300  
QY 97 LeuThrAsnHisLysValIlyrGlyGluTyrThrAlaLeuAlaGlyAspAlaLeuLeu 116  
Db 301 CCGAGAACCATTAAGCTTCGCGGACGCGATGCCATCTTGCGCGGAGAGGATTTG 360  
QY 117 ThrLysAlaPheGluLeuileSer-----SerAspArgLeuThrAspGluValLys 134  
Db 361 ACGTACGCGTTTCATTCATTCATCCGAATCGACGATGACGATCCCTCCGTCGCG 420  
QY 135 IlaLysValLeuGlnArgLeuSerIlaLysSerGlyIleValGlyMetValGlyGln 154  
Db 421 CTTCGCTCATCGAACGCGCTGCGAAGCGCGCTCCGAGGAGATGCGCGCGCTACG 480  
QY 155 MetLeuAspMetGlnSerGluGlyGlnProIleAspLeuGluThrLeuGluMetLeuHis 174  
Db 481 GCAGCCGATATGAGAGAGAGAGCGGAAAAACGTGACGCTTCGAGGCTCGAATATCATTCAT 540  
QY 175 LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIlaAspIleAlaAsn 194  
Db 541 CGGTATTAACCGCGGAAAAATGCTGCATACAGCGCTGACCGCGCGCTTCGATCGCGCGC 600  
QY 195 ValAspAspThrThrLysGluHisLeuGluSerTyrSerTyrHisLeuGlyMetMetPhe 214  
Db 601 GCTATGCGCGGCAAGCGGAGCTTGACGAATTCGCCGCCCATCTAGCGCTTCGCTTT 660  
QY 215 GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGluAlaLysLeuGlyLysVal 234  
Db 661 CAATTCGCGCATGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 720  
QY 235 GlySerAspLeuGluAsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyVal 254  
Db 721 GCGAGCGACCAACGACCAACGACGATTCACGCTTCGCTGCTGCTGCTGCTGCTGCTGCTG 780  
QY 255 GluAspLysLeuThrTyrHisArgAspAlaAlaValAspGluLeuThrGlnIleAsp 273  
Db 781 AAGAAAAGTTGGCTTCATATGAGCGCGAGCCGCAATTACGAAAGCCGAC 837

RESULT 9  
US-08-886-466-1  
Sequence 1, Application US/08886466C  
Patent No. 6040165

GENERAL INFORMATION:  
APPLICANT: Narita, Keishi  
APPLICANT: Ishida, Chika  
APPLICANT: Takeuchi, Yoshie  
APPLICANT: Ohto, Chikara  
APPLICANT: Ohnuma, Shinichi  
APPLICANT: Nishino, Tokuzo  
TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE  
FILE REFERENCE: 77670/494  
CURRENT APPLICATION NUMBER: US/08/886,466C  
EARLIER FILING DATE: 1997-07-10  
EARLIER APPLICATION NUMBER: JP 8-191635  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 1  
LENGTH: 894  
TYPE: DNA  
ORGANISM: *Bacillus stearothermophilus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(891)

US-08-886-466-1

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
7.52e-74	650.00	67.78%	49.63%	44.74%	894	134	49	85	2	1

US-09-925-637-64 (1-287) x US-08-886-466-1 (1-894)

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QY 6 MetAspLeuIleAspGluValAsnGluSerValAlaIleAsnLysSerVal 25
DB 28 CTCACGACGCAAAACAGCGCGTGGAAACAGCGCTCTCCGTTATATAGACCGCTTAGA 87
QY 26 MetAspThrGluIleGluIleGluSerMetLeuTyrSerLeuAsnAlaGlyGlyArgGly 45
DB 88 GGGCGCGGCAAGCTGAAAGGCGATGCGATCTCATTCATGAGCGCGCGCAACGATC 147
QY 46 ArgProValIleLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGluGlyMet 65
DB 148 CGTCGGTTGCTGCTTCTGTCACCGCTTCGCGCGCTCGCAAGACCGCGCGCGATG 207
QY 66 LysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspAspLeuPro 85
DB 208 CCCGTCGCTGCGCGGATGAAATGATCATACGATCTTGTATCCATGATGATTCGCG 267
QY 86 AlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlyGlu 105
DB 268 AGCATGACACATGATGATTCGCGCGCGCAAGCGACGACCAACCAATTAAGTTCGCGAG 327
QY 106 TrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSer--- 124
DB 328 GCGATGCGCATCTTGGCGGGAAGCGGTGTTGACGATGACGATTCATTAATGATCAGCA 397
QY 125 ---SerAspAspArgLeuThrAspGluValIleLysValLeuGluArgLeuSerIle 143
DB 388 ATCAGCATGAGCGCATCCCTCCCTCCGCTTCGCGCTTCATCGAAGCGCTGCGCAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyGlyIleMetLeuAspMetGlnSerGlyGln 163
DB 448 GCGCGCGGTCGCGAAGGATGTCGCGCGTACGACGATGATGAGAGAGAGGCGGAAA 507
QY 164 ProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThr 183
DB 508 AGCGTACGCTTTCGAGCTCGAATCATCTCATCGCATTAACCGGAAATGCTGCA 567
QY 184 PheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrThrLysGluHisLeu 203
DB 568 TACAGCGTACGCGCGCGCTTATGCGCGCGCTGATGCCCGCAACCGCGGAGCTT 627
QY 204 GluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuAspCys 223
DB 628 GACGATTCGCGCGCGCATGAGCTTCGCTTCATCAATTCGCGATGATTCGATATT 687
QY 224 TyrGlyAspGluAlaLysLeuGlyLysLysValGlySerAspLeuGluAsnLysSer 243
DB 688 GAGGCGGCAAGAAAGAAATCGCGCAAGCGGTCGCGACGACCAACGACAAAGAAACG 747
QY 244 ThrTyrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisAsp 263
DB 748 ACGTATCCAGCGTTCGCTTCGCTTCGCGCGCGCAAGAAAGTTCGCTTCATATCGAG 807
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273
DB 808 GCGCGCAAGCGCATTTACGAGAACCGCAC 837

```

RESULT 10

US-09-475-304-1  
 ; Sequence 1, Application US/09475304  
 ; Patent No. 6225096  
 ; GENERAL INFORMATION:

```

/ APPLICANT: Narita, Keishi
/ APPLICANT: Ishida, Chika
/ APPLICANT: Takeuchi, Yoshie
/ APPLICANT: Ohts, Chikara
/ APPLICANT: Ohnuma, Shinichi
/ APPLICANT: Nishino, Tokuzo
/ TITLE OF INVENTION: MOTANT PRENYL DIPHOSPHATE SYNTHASE
/ FILE REFERENCE: 77670/494
/ CURRENT APPLICATION NUMBER: US/09/475,304
/ EARLIER FILING DATE: 1999-12-30
/ EARLIER APPLICATION NUMBER: JP 8-191635
/ EARLIER FILING DATE: 1996-07-03
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 894
/ TYPE: DNA
/ ORGANISM: Bacillus stearothermophilus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(891)
/ US-09-475-304-1

```

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
7.52e-74	650.00	67.78%	49.63%	44.74%	894	134	49	85	2	1

US-09-925-637-64 (1-287) x US-09-475-304-1 (1-894)

```

QY 6 MetAspLeuIleAspGluValAsnGluSerValAlaIleAsnLysSerVal 25
DB 28 CTCACGACGCAAAACAGCGCGTGGAAACAGCGCTCTCCGTTATATAGACCGCTTAGA 87
QY 26 MetAspThrGluIleGluIleGluSerMetLeuTyrSerLeuAsnAlaGlyGlyArgGly 45
DB 88 GGGCGCGGCAAGCTGAAAGGCGATGCGATCTCATTCATGAGCGCGCGCAACGATC 147
QY 46 ArgProValIleLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGluGlyMet 65
DB 148 CGTCGGTTGCTGCTTCTGTCACCGCTTCGCGCGCTCGCAAGACCGCGCGCGATG 207
QY 66 LysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspAspLeuPro 85
DB 208 CCCGTCGCTGCGCGGATGAAATGATCATACGATCTTGTATCCATGATGATTCGCG 267
QY 86 AlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlyGlu 105
DB 268 AGCATGACACATGATGATTCGCGCGCGCAAGCGACGACCAACCAATTAAGTTCGCGAG 327
QY 106 TrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSer--- 124
DB 328 GCGATGCGCATCTTGGCGGGAAGCGGTGTTGACGATGACGATTCATTAATGATCAGCA 387
QY 125 ---SerAspAspArgLeuThrAspGluValIleLysValLeuGluArgLeuSerIle 143
DB 388 ATCAGCATGAGCGCATCCCTCCCTCCGCTTCGCGCTTCATCGAAGCGCTGCGCAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyGlyIleMetLeuAspMetGlnSerGlyGln 163
DB 448 GCGCGCGGTCGCGAAGGATGTCGCGCGTACGACGATGATGAGAGAGAGGCGGAAA 507
QY 164 ProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThr 183
DB 508 AGCGTACGCTTTCGAGCTCGAATCATCTCATCGCATTAACCGGAAATGCTGCA 567
QY 184 PheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrThrLysGluHisLeu 203
DB 568 TACAGCGTACGCGCGCGCTTATGCGCGCGCTGATGCCCGCAACCGCGGAGCTT 627

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QY 204 GlnSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLeuAspAspLeuLeuAspCys 223
    ::::::::::::::::::::
Db 628 GACGAATTCGCCGCCATCTAGCGCTTGCTTCAAAATCCGAGATGATTTCTGCATATT 687
QY 224 TyrGlyAspGluAlaLeuLeuGlyLysValGlySerAspLeuGluAsnLysSer 243
    ::::::::::::::::::::
Db 688 GAAGGGCGCAAGAAAAATCGCAGACCGGTCCGCGAGGACCAAGCAACAAACGCG 747
QY 244 ThrTyrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAsp 263
    ::::::::::::::::::::
Db 748 ACGTATCCAGCGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCT 807
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273
    ::::::::::::::::::::
Db 808 GCGGCGCAGCGCCATTACGAGACGCCGAC 837

RESULT 11
US-09-101-126-4
/ Sequence 4, Application US/09101126
/ Patent No. 6316216
/ GENERAL INFORMATION:
/ APPLICANT: OHTO, CHIKARA
/ APPLICANT: NAKANE, HIROYUKI
/ APPLICANT: NISHINO, TOKUZO
/ APPLICANT: OHMURA, SHINICHI
/ APPLICANT: HIROOKA, KAZUTAKE
/ TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES
/ FILE REFERENCE: 77670/566
/ CURRENT APPLICATION NUMBER: US/09/101,126
/ EARLIER FILING DATE: 1999-04-27
/ EARLIER APPLICATION NUMBER: PCT/JP97/03921
/ EARLIER FILING DATE: 1997-10-29
/ EARLIER APPLICATION NUMBER: JP 8-307506
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 894
/ TYPE: DNA
/ ORGANISM: Bacillus stearothermophilus
/ FEATURE:
/ OTHER INFORMATION: 256-276 is an Asp-rich coding domain
US-09-101-126-4

Alignment Scores:
Pred. No.: 7,52e-74 Length: 894
Score: 650.00 Matches: 134
Percent Similarity: 67.78% Conservative: 49
Best Local Similarity: 49.63% Mismatches: 85
Query Match: 44.74% Indels: 2
DB: Gaps: 1

US-09-925-637-64 (1-287) x US-09-101-126-4 (1-894)
QY 6 MetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAlaIleAsnLysSerVal 25
    ::::::::::::::::::::
Db 28 CTCACAGACGCAAAAACAGCGCGGTGAAAACAGCGCTCTCCGTTATATAGAGCGCTTAA 87
QY 26 MetAspThrGlnLeuGlnGluSerMetLeuTyrSerLeuAsnAlaGlyLysArgIle 45
    ::::::::::::::::::::
Db 88 GGGCGCGCGCAAGTAAAGCGGAGTGGGCTGCTCATTTGAGAGCGCGCGCAACGAAATC 147
QY 46 ArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGluLeuGlyMet 65
    ::::::::::::::::::::
Db 148 CCGTCGCTGCTCTCTGTCACCGTTCGCGCGCTCGGCAAGAACCGCGCGTTCGATG 207
QY 66 LysSerAlaIleAlaLeuGluValMetIleHisThrTyrSerLeuIleHisAspAspLeuPro 85
    ::::::::::::::::::::
Db 208 CCCGTCGCTGCGCATTTGAATGATCCATGACTCTTTGATCATGATGATTTGCGG 267
QY 86 AlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnIleLysValTyrGlyGlu 105
    ::::::::::::::::::::
Db 268 AACAATGACAAAGATGATTTGCGCGCGCAAGCGCAAGAACCAATAAAGTGTTCGCGCAG 327
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QY 106 TrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSer--- 124
    ::::::::::::::::::::
Db 328 GCGATGCCATCTTGCGGGGGGACCGGTTCTTACGACCGCTTCAATTCATTCATCACCGAA 387
QY 125 ---SerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArgLeuSerIle 143
    ::::::::::::::::::::
Db 388 ATCGACGATAGCGCATCCCTCCCTCCGCTTCGCTCATCGAACCGCTGCGCAAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyGlnMetLeuAspMetGlnSerGlnIleGln 163
    ::::::::::::::::::::
Db 448 GCGCCGCTCGGAGAGGATGTCGCCGTCACGACCGCATATGAGAGAGGGGAAA 507
QY 164 ProLeuAspLeuGlnThrLeuGluMetIleHisLysThrTyrThrGlyAlaLeuLeuThr 183
    ::::::::::::::::::::
Db 508 ACGCTGACGCTTCGGAGCTCGAATCATTCATCGGATTAACCGGAAAAATGCTGCAA 567
QY 184 PheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrThrLysGluHisLeu 203
    ::::::::::::::::::::
Db 568 TACGCGTGCACCGCGCGCTTGATCGCGCGCTGATGCCCCGCAACCGCGGAGCTT 627
QY 204 GlnSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuLeuAspCys 223
    ::::::::::::::::::::
Db 628 GACGAATTCGCCGCCATCTAGCGCTTGCTTCAAAATCCGAGATGATTTCTGCATATT 687
QY 224 TyrGlyAspGluAlaLeuLeuGlyLysValGlySerAspLeuGluAsnLysSer 243
    ::::::::::::::::::::
Db 688 GAAGGGCGCAAGAAAAATCGCAGACCGGTCCGCGAGGACCAAGCAACAAACGCG 747
QY 244 ThrTyrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAsp 263
    ::::::::::::::::::::
Db 748 ACGTATCCAGCGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCT 807
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273
    ::::::::::::::::::::
Db 808 GCGGCGCAGCGCCATTACGAGACGCCGAC 837

RESULT 12
US-09-367-528A-4
/ Sequence 4, Application US/09367528A
/ Patent No. 6395525
/ GENERAL INFORMATION:
/ APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
/ TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene
/ FILE REFERENCE: PH-586
/ CURRENT APPLICATION NUMBER: US/09/367,528A
/ EARLIER FILING DATE: 1999-08-16
/ PRIOR APPLICATION NUMBER: JP97/346686
/ EARLIER FILING DATE: 1997-12-16
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 894
/ TYPE: DNA
/ ORGANISM: Bacillus stearothermophilus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(894)
US-09-367-528A-4

Alignment Scores:
Pred. No.: 7,52e-74 Length: 894
Score: 650.00 Matches: 134
Percent Similarity: 67.78% Conservative: 49
Best Local Similarity: 49.63% Mismatches: 85
Query Match: 44.74% Indels: 2
DB: Gaps: 1

US-09-925-637-64 (1-287) x US-09-367-528A-4 (1-894)
QY 6 MetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAlaIleAsnLysSerVal 25
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Db 28 CTCACAGACGCAAAAACAGCGCGGTGAAAACAGCGCTCTCCGTTATATAGAGCGCTTAA 87
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QY 26 MetAspThrGlnLeuGluGluSerMetLeuTyrSerLeuAsnAlaGlyLysArgIle 45
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Db 88 GGGCCGGCGGAGTGAAGAAAGCGGATGGCGTACTCATTTGAGGCGCGGCGGCAACGAAATC 147
QY 46 ArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGlnTyrGlnLeuGlyMet 65
   ::::::::::::::::::::
Db 148 CGTCCGTGCTGCTTCTGTCACCGCTCCGCGCGCTGGCAAGAACCGCGCGGTGGATTTG 207
QY 66 LysSerAlaIleLeuLeuGluMetLeuIleAsnThrTyrSerLeuIleHisAspLeuPro 85
   ::::::::::::::::::::
Db 208 CCGGTGGCTGGCGCGGATGTAAGATGATCCATAGCTACTCTTTATTCATGATGTTTGGCG 267
QY 86 AlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlyGln 105
   ::::::::::::::::::::
Db 268 AGCATGGACAAACATGATTTGGCGGCGGCGGCAACCCGCAACCATTAAGTTTCGGCGAG 327
QY 106 TyrThrAlaIleLeuAlaGlyAspAlaLeuLeuThrTyrAlaAspGluLeuIleSer--- 124
   ::::::::::::::::::::
Db 328 GCGATGGCCATCTTGGCGGCGGAGCGGCTTGTACGATGCGCTTCAATTGATTCACCGAA 387
QY 125 ---SerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArgLeuSerIle 143
   ::::::::::::::::::::
Db 388 ATCGACGATGAGCGCATCCCTCCCTCCGCTCGGCTTCGCTCATCGAACGCGTGGCGGAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSerGluGln 163
   ::::::::::::::::::::
Db 448 GCGGCGCGTCCGGAAGGATGTGTCCCGGTCAGCGCACCGCATTTGAGAGAGAGGAGGAA 507
QY 164 ProIleAspLeuGluThrLeuGluMetIleHisLysThrTyrSerThrGlyAlaLeuLeuThr 183
   ::::::::::::::::::::
Db 508 ACGGTGACGCTTTCGAGCGTGAATCATTCATCGGCAATAAAACCGGAAATGCTGCAG 567
QY 184 PheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrTyrSerGluHisLeu 203
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Db 568 TACAGCGCTGACCGCGCGCTTGTATCGCGGCGCTGATGCCCGGCAACCGCGGAGCTT 627
QY 204 GluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuAspCys 223
   ::::::::::::::::::::
Db 628 GACGAATTCGCCCGCCATCTAAGCGCTTCCCTTCAATTCCGATATTTCCGATATT 687
QY 224 TyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGluMetLeuHisSer 243
   ::::::::::::::::::::
Db 688 GAAAGGCGCAGAAAGAAATCGCGACCGGTCGCGAGCGCAACCAACCAAGAGCG 747
QY 244 ThrTyrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAsp 263
   ::::::::::::::::::::
Db 748 ACGATGCCAGCGTTCGTGCGCTTCCGCGCGGAGAGAAAGTTGGCGTTCCATATCGAG 807
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273
   ::::::::::::::::::::
Db 808 GCGCGCGCAGCGCCATTTACGAAACGCGGAC 837

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# RESULT 13 US-08-534-910B-1

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Sequence 1, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: KOYAMA, Tanetoshi
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC

```

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COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
CLASSIFICATION: 435
FILING DATE: 28-SEPT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Tofteneck, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-1

Alignment Scores:
Pred. No.: 3,3e-73 Length: 894
Score: 645.00 Matches: 130
Percent Similarity: 68.63% Conserves: 56
Best Local Similarity: 47.97% Mismatches: 79
Query Match: 44.39% Indels: 6
DB: 1 Gaps: 2

US-09-925-637-64 (1-287) X US-08-534-910B-1 (1-894)
QY 1 MetThrAsnLeuProMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
   ::::::::::::::::::::
Db 1 ATGGCGCAGCTTATGATGAGCAAGTTCTCAACGAGCAAAACAGCGGAGGAAACGCG 60
QY 21 IleAsnLysSerValMet-----AspThrGlnLeuGluGluSerMetLeuTyr 36
   ::::::::::::::::::::
Db 61 CTCGCCGTATATAGAGCGCTTAGAAGGCGCGCGGCGGCAAGCGATGCGGTAC 120
QY 37 SerLeuAsnAlaGlyLysArgIleArgProValLeuLeuLeuLeuThrLeuAspSer 56
   ::::::::::::::::::::
Db 121 TCATTGGAGCGCGCGGCAACGATCCGTCCTGCTGTCACCGCTTCGCGAGCG 180
QY 57 LeuAsnThrGluTyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThr 76
   ::::::::::::::::::::
Db 181 CTCGGAAGAAAGCCCGCGCGGTGGATTGCGCCCTCGCGCGGATGTAATGATCATACG 240
QY 77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96
   ::::::::::::::::::::
Db 241 CACCTTTGATCCATGATGATTTGCCAGATGACAGCAACGATGATTTGGCGCGCGGCAAG 300
QY 97 LeuThrAsnHisLysValTyrGlyGluThrPheAlaIleLeuAlaGlyAspAlaLeuLeu 116
   ::::::::::::::::::::
Db 301 CCGAGAACCAATTAAGTTTGGCGAGCGCATGCGCATCTTGGCGGCGGAGCGGTGTG 360
QY 117 ThrLysAlaPheGluLeuLeuSer-----SerAspAspArgLeuThrAspGluValLys 134
   ::::::::::::::::::::
Db 361 ACGTACGCGTTCAATTGATGATCCGAAATCGACCATAGACCATCTCTTCGTCGCGG 420
QY 135 IleLysValLeuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
   ::::::::::::::::::::
Db 421 CTTCGCTCATCGAACGCGTGGCAAGCGCGCGCTCCGGAAGGAGATGCTGCGCGGTACG 480

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QY 155 MetLeuAspMetGlnSerGluGlnProIleAspLeuGluThrLeuGluMetIleHis 174  
DB 481 GCAGCCGATATGGAAGGAGGAGAAACGCTGACGCTTCGAGCTTGAATACATTCAT 540  
QY 175 LysThrLysThrGluValAlaLeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsn 194  
DB 541 CGGCAATAAACCGGGAATATGCTGCATATACAGCGTGCACGCGCGGCTTATCGCGGCG 600  
QY 195 ValAspAspThrThrLysGluLysIleLeuGluSerTyrosThrLysLeuGluMetMetHe 214  
DB 601 GCTGATGCCCGGCAACGCGGAGCTTGACGAATTCGCGCCCATCTAGGCTTGCCTTT 660  
QY 215 GlnIleLysAspAspLeuLeuAspCysTyrosGlyAspGluAlaLysLeuGluLysLysVal 234  
DB 661 CAATTCGCGATGATATTCCTCATATGTGAAGGCGGAGAAAGAAATCGCAAGCGCTC 720  
QY 235 GlySerAspLeuGluAsnAsnLysSerThrTyrosValSerLeuLeuGluLysAspGluVal 254  
DB 721 GCGAGCGACCAAGCAACAACAAAGCGAGCTATCCAGCGCTGCTGCTGCGCGCGG 780  
QY 255 GluAspLysLeuThrTyrosHisArgAspAlaIle 265  
DB 781 AAGGAAAGTTGGCGCTTCATATCGAGCGCGG 813

## RESULT 14

US-09-367-528A-2  
Sequence 2, Application US/09367528A  
Patent No. 635525  
GENERAL INFORMATION:  
APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA  
TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene  
FILE REFERENCE: PH-586  
CURRENT APPLICATION NUMBER: US/09/367,528A  
PRIOR FILING DATE: 1999-08-15  
CURRENT FILING DATE: 1997-12-16  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 894  
TYPE: DNA  
ORGANISM: Bacillus stearothermophilus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(894)  
US-09-367-528A-2

## Alignment Scores:

Pred. No.: 4,43e-73 Length: 884  
Score: 644.00 Matches: 133  
Percent Similarity: 67.41% Conservative: 49  
Best Local Similarity: 49.26% Mismatches: 86  
Query Match: 44.32% Indels: 2  
Gaps: 1

US-09-925-637-64 (1-287) x US-09-367-528A-2 (1-894)

QY 6 MetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAlaIleAsnLysSerVal 25  
DB 28 CTCACGACGACAAACAGCGCGGTGGAACAGCGCTTCCGTTATATAGAGCGCTTAGA 87  
QY 26 MetAspThrGlnLeuGluGlnLysMetLeuTyrosSerLeuAsnAlaGlyLysArgIle 45  
DB 88 GGGCCCGGCGAAGCTGAAAAGCGATGCGCTACTCATGTGAGCGCGCGCAACGATC 147  
QY 46 ArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrosGluLeuGlyMet 65  
DB 148 CGTCCGCTGCTGCTTCGTCACCGTTCGCGCGCTCGGCAAGACCGGCGGTGATG 207  
QY 66 LysSerAlaIleLeuGluMetIleHisThrTyrosSerLeuIleHisAspLeuPro 85  
DB 208 CCCGTCGCGCGATGAAATGATCATCATCTTCTTGATCATATGATGATTTGCGG 267

QY 86 AlaMetAspAsnAspAspTyrosArgArgGlyLysLeuThrAsnHisLysValTyrosGlu 105  
DB 268 AGCATGACACACATGATTTTCCGCGCGGACCGACCGACCAACCATTAAGTTTCGCGGAG 327  
QY 106 TrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSer 124  
DB 328 GCGATGCCATCTTGGGGGGGACGGGTTGTACGATACCGCTTCATATGATGATCACCAG 387  
QY 125 ---SerAspAspArgLeuThrAspGluValLysIleLysValLeuGluAlaGlySerIle 143  
DB 388 ATCGACGATGAGGACATCCCTCTCCGCTCGGCTTCGCTCATCGAACGCTGCGCAA 447  
QY 144 AlaSerGlyHisValGlyMetValGlyGlnMetLeuAspMetGlnSerGluGln 163  
DB 448 GCGGCGCGTCCGGAAGGATGTCGCGGTCAGGACGATATGAGAGGAGGAGAA 507  
QY 164 ProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThr 183  
DB 508 ACGCTGACGCTTCGAGCTCGAATCATTCATCGGATTAACCGGAAAAAGCTGCAA 567  
QY 184 PheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisLeu 203  
DB 568 TACAGCGTCACCGCGCGGCTTGATGCGGCGCTGATCCCGGCAACGCGGAGCTT 627  
QY 204 GluSerTyrosThrLysLeuGluMetMetPheGlnIleLysAspAspLeuAspCys 223  
DB 628 GACGAATTCGCGCGCCCATATGAGCTTGCCTTCAATTCGATATTCGATATT 687  
QY 224 TyrGlyAspGluAlaLysLeuGluLysLysValGlySerAspLeuGluAsnAsnLysSer 243  
DB 688 GAAAGGCGACAAAGAAATCGGACACCGCTGCGGACGACCAACCAACCAACG 747  
QY 244 ThrTyrosAlaSerLeuLeuGluLysAspGlyAlaGluAspLysLeuThrTyrosArgAsp 263  
DB 748 ACGATCCAGCGTTGCTGCTGCTGCGCGCGGAGGAAAGTTGGCTTCATATCGAG 807  
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273  
DB 808 GCGGCGACGCGCATTTACGAAACGCGAC 837

## RESULT 15

US-09-275-742-1  
Sequence 1, Application US/09275742  
Patent No. 6130069  
GENERAL INFORMATION:  
APPLICANT: Wilding, Edwin Imogen  
APPLICANT: Gwynn, Michael  
TITLE OF INVENTION: Ispa  
FILE REFERENCE: GM10205  
CURRENT APPLICATION NUMBER: US/09/275,742  
PRIOR FILING DATE: 1999-03-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 876  
TYPE: DNA  
ORGANISM: Streptococcus pneumoniae  
US-09-275-742-1

## Alignment Scores:

Pred. No.: 3.72e-61 Length: 876  
Score: 551.00 Matches: 122  
Percent Similarity: 64.89% Conservative: 48  
Best Local Similarity: 46.56% Mismatches: 88  
Query Match: 37.92% Indels: 4  
Gaps: 3

US-09-925-637-64 (1-287) x US-09-275-742-1 (1-876)

QY 28 ThrGlnLeuGluGlnLysMetLeuTyrosSerLeuAsnAlaGlyLysArgIleArgPro 47  
DB 73 TCTAGTTACCGGAGTCTGTTCTCTATTCATATCATGCTGTGCAAGCGATTCGCGCT 132



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QY 48 ValLeuLeuLeuThrLeuAspSerLeuAsn---ThrGluTyrGluLeuGlyMetLys 66
Db 133 TTTCCTCTGTAAAGCTTCTGGAAGCTTGCAGGTTACCATCAAACTGCTCAGCGGAG 192
QY 67 SerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspAspLeuProAla 86
Db 193 GTAGCTACTGCTTGAAGATGATTCATACAGGAGCTGATTCACGATGACCTTCTGCT 252
QY 87 MetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisIleValTyrGlyGluTrp 106
Db 253 ATGGATGATGACGATTCAGAAAGGCGGCTTACCAATCACAGAAATTCGGTAGCT 312
QY 107 ThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSerSerAsp 126
Db 313 ATGGCCATTTTGGCTGAGATGCTTATCTTATAGACCATATGCTGATTCGCGAGGCA 372
QY 127 AspArgLeuThrAspGluValLysIleLysValLeuGlnArgLeuSerIleAlaSerGly 146
Db 373 GAT---TTGCCAAGTCAGATCAAGGCGGCTTGATGCCAAGCTTATCCTTCTCAGGT 429
QY 147 HisValGlyMetValGlyGlyMetLeuAspMetGlnSerGluGlnProIleAsp 166
Db 430 AGTCTGGGTTGTGGCAGGCGCAAGTTTGATATGAGAGGCGAACAACGACCTTGCT 489
QY 167 LeuGluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThrPheAlaVal 186
Db 490 CTGGAAAGACTTCAGACTATTCATGCCAATTAAGCTGGAGTACTAGCTATCCCTTC 549
QY 187 MetSerAlaIleAspIleAlaAsnValAspAspThrThrLysGluHisLeuGluSerTyr 206
Db 550 CAAGCGGACGCTTATAGCTGAATGTCACTGAATGCAAGGTGAAGCTGAAGAACTGTG 609
QY 207 SerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuAspCysTyrGlyAsp 226
Db 610 GGTGAATTTGATGACTTGTCTTTCAAGTCAGAGATGATGATCTGATGTACGGCTAGT 669
QY 227 GluAlaLysLeuGlyLysLysValGlySerAspLeuGluAsnLysSerThrTyrVal 246
Db 670 TTGAGGAAATCGGCAAGACACCTCAAAAGGATCTGCGGCGAGAAAATCAACCTATCCT 729
QY 247 SerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAspAlaAlaVal 266
Db 730 GCCTTGTGGCTTGGAGAAGCTCATTCCTTTGTAAACCAACCTGGATCAAGCTAAT 789
QY 267 AspGluLeuThrGlnIleAspGluGln-----PheAsnThrLysHisLeuLeuGluIle 284
Db 790 GATTAATTAGAAATTTGCCAGACGACTTCCTTTGAAACAGAAATCGATTGTAAAGTGA 849
QY 285 ValAsp 286
Db 850 GTAGAA 855
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Job time : 77 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 20, 2004, 11:17:59 ; Search time 389 seconds  
(without alignments)  
3301.297 Million cell updates/sec

Title: US-09-925-637-64  
Perfect score: 1453  
Sequence: 1 MTNLPNKLDEVNNELSVA.....ELQIDQFVTKLEIVDL 287

Scoring table:  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgn2\_1/USPFO.epool.p/US09925637/runtat.19042004.140331.25275/app.query.fasta\_1.455  
-DB=Published Applications NA -QFMT=fastcap -SUFFIX=trmp -MTNMATCH=0.1  
-DOFCL=0 -LOOPEXT=0 -UNITS=Dits -START=1 -END=1 -MATRIX=blonum2  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NOM=ext -HAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09925637 @CGN 1.1 333 @runtat.19042004.140331.25275  
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-NCLIOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.\*  
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19: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARY

Result Query Match Length DB ID Description

1	1453	100.0	861	9	US-09-925-637-63	Sequence 63, Appl
2	1453	100.0	861	15	US-10-084-205-63	Sequence 63, Appl
3	1453	100.0	1893	8	US-08-781-986A-155	Sequence 155, Appl
4	1453	100.0	1893	13	US-10-328-624-155	Sequence 155, Appl
5	1444	99.4	882	13	US-10-282-122A-8179	Sequence 8179, Appl
6	1442	99.2	882	9	US-09-815-242-8485	Sequence 8485, Appl
7	1415	97.4	864	9	US-09-815-242-4184	Sequence 4184, Appl
8	1040	71.6	879	13	US-10-282-122A-35068	Sequence 35068, Appl
9	1015	69.9	879	13	US-10-282-122A-34531	Sequence 34531, Appl
10	702.5	48.3	882	13	US-10-282-122A-24756	Sequence 24756, Appl
11	693.5	47.9	5635	16	US-10-398-221-8823	Sequence 3823, Appl
12	690	47.5	413	9	US-09-815-242-2822	Sequence 2822, Appl
13	690	47.5	413	13	US-10-282-122A-5390	Sequence 5390, Appl
14	686.5	47.2	495269	16	US-10-398-221-8	Sequence 2058, Appl
15	686.5	47.2	3011208	16	US-10-398-221-2058	Sequence 75, Appl
16	650	44.7	894	13	US-10-462-658A-75	Sequence 41045, Appl
17	638	43.9	885	16	US-10-369-493-41045	Sequence 1015, Appl
18	635	43.7	811	9	US-09-874-300-1015	Sequence 46888, Appl
19	632.5	43.5	819	16	US-10-369-493-46888	Sequence 40236, Appl
20	617	42.5	888	13	US-10-369-493-40236	Sequence 9306, Appl
21	615	42.3	888	13	US-10-282-122A-9306	Sequence 21105, Appl
22	596	41.0	879	13	US-10-282-122A-21105	Sequence 6533, Appl
23	596	41.0	882	9	US-09-815-242-6533	Sequence 55, Appl
24	587.5	40.4	7828	9	US-09-070-927A-55	Sequence 33397, Appl
25	578.5	39.8	783	16	US-10-369-493-33397	Sequence 3271, Appl
26	570	39.2	337	9	US-09-815-242-3275	Sequence 3275, Appl
27	570	39.2	337	13	US-10-282-122A-3275	Sequence 17062, Appl
28	568	39.1	885	13	US-10-282-122A-17062	Sequence 16522, Appl
29	567	38.9	882	13	US-10-282-122A-16522	Sequence 44580, Appl
30	566	38.3	870	16	US-10-369-493-44580	Sequence 36078, Appl
31	552	38.0	867	13	US-10-282-122A-36078	Sequence 38458, Appl
32	551.5	38.0	873	13	US-10-282-122A-38458	Sequence 9499, Appl
33	549	37.8	876	9	US-09-815-242-9499	Sequence 76, Appl
34	549	37.8	10011	13	US-10-158-844-76	Sequence 9176, Appl
35	547	37.6	876	9	US-09-815-242-9175	Sequence 37814, Appl
36	547	37.6	876	13	US-10-282-122A-37814	Sequence 42078, Appl
37	544.5	37.5	930	16	US-10-369-493-42078	Sequence 42078, Appl
38	540.5	36.8	858	16	US-10-369-493-42439	Sequence 152439, Appl
39	534.5	36.8	927	16	US-10-282-122A-15342	Sequence 26295, Appl
40	532	36.6	870	13	US-10-282-122A-26295	Sequence 32193, Appl
41	526.5	36.2	909	16	US-10-369-493-32193	Sequence 21259, Appl
42	524	36.1	873	16	US-10-369-493-32193	Sequence 13, Appl
43	520.5	35.8	795	13	US-10-282-122A-21259	Sequence 71, Appl
44	516.5	35.5	891	9	US-09-934-903-13	
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## ALIGNMENTS

RESULT 1  
US-09-925-637-63  
Sequence 63, Application US/09925637  
Patent No. US2002010338A1  
GENERAL INFORMATION:  
APPLICANT: Chai  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides  
FILE REFERENCE: PB560  
CURRENT APPLICATION NUMBER: US/09/925, 637  
PRIOR APPLICATION NUMBER: PCT/US00/22773  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US 60/151,933  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: US 08/781,986  
PRIOR FILING DATE: 1997-01-03  
PRIOR APPLICATION NUMBER: US 08/956,171  
PRIOR FILING DATE: 1997-10-20  
PRIOR APPLICATION NUMBER: US 60/009,861  
PRIOR FILING DATE: 1996-01-06  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 63

Tue Apr 20 12:43:40 2004

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Page 2

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; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-637-63

Alignment Scores:
Pred. No.: 6,686-162 Length: 861
Score: 1453.00 Matches: 287
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-925-637-64 (1-287) x US-09-925-637-63 (1-861)

QY 1 MetThrsAsnLeuProMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
DB 1 ATGACGATCTACCGATGGAATTAATTAATGATGATCAATGATCAATTAATCGGTGGC 60
QY 21 IleAsnLysSerValMetAspThrGluLeuGluGluSerMetLeuTyrSerLeuAsnAla 40
DB 61 ATAATAATTAATCTAGTAAGATGATCTACGTAAGAAAGTAAGTGTGATTAATCAATTAATGCT 120
QY 41 GlyGlyLysArgIleArgProValLeuLeuLeuThrLeuAspSerLeuAsnThrGlu 60
DB 121 GGAGGTAAACCAATCCGACCGACGATCTGTTATTACTCACTTAAGATTCACTAAATACCGAG 180
QY 61 TyrGluLeuGluMetLysSerValIleAlaLeuGluMetIleHisThrTyrSerLeuIle 80
DB 181 TATAGTATGAGTAAAGAAAGCGCAATTCACATAAATGATTCATCAATTAATCACTTAAT 240
QY 81 HisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHis 100
DB 241 CATATGACCTACACGATGATGATTAATGATTAATGATGATGATTAATGATTAATGATTAAT 300
QY 101 LysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120
DB 301 AAAGTAATGAGTGTGATGATGATGATTAATGATTAATGATTAATGATTAATGATTAAT 360
QY 121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGluArg 140
DB 361 GAACTTATTTCAAGTATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 420
QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSer 160
DB 421 CTGCAATAGCAAGTGTGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 480
QY 161 GluGlyGlnProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAla 180
DB 481 GAAGGCCAACCAATGATCTTGAAACTTTGAAATGATACAAACAAACAAACGAGGCA 540
QY 181 LeuLeuThrPheAlaValMetSerAlaIleAspIleAsnValAspAspThrThrLys 200
DB 541 TTATTAATCTTTGCGGTTATGATGATGATTAATGATTAATGATTAATGATTAATGATTAAT 600
QY 201 GlnHisLeuGluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeu 220
DB 601 GAACCTTTAGAAAGTATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 660
QY 221 LeuAspCysTyrGlyAspGluAlaLysLeuGlyLysLysValGlySerAspLeuGluAsn 240
DB 661 TTAGCTGCTATGCGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 720
QY 241 AsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyr 260
DB 721 AATAAAAGTACGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 780
QY 261 HisAspAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
DB 781 CATAGACGACGACGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 840
QY 281 LeuLeuGluIleValAspLeu 287
|||||
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DB 841 TTATTAAGAAATCGTTGATTTA 861

RESULT 2
US-10-084-205-63
; Sequence 63, Application US/10084205
; Publication No. US20030049648A1
; GENERAL INFORMATION:
; APPLICANT: ChOI, Gil
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: PB515P1
; CURRENT APPLICATION NUMBER: US/10/084,205
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 63
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-084-205-63

Alignment Scores:
Pred. No.: 6,686-162 Length: 861
Score: 1453.00 Matches: 287
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-925-637-64 (1-287) x US-10-084-205-63 (1-861)

QY 1 MetThrsAsnLeuProMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
DB 1 ATGACGATCTACCGATGGAATTAATTAATGATGATGATTAATGATTAATCGGTGGC 60
QY 21 IleAsnLysSerValMetAspThrGluLeuGluGluSerMetLeuTyrSerLeuAsnAla 40
DB 61 ATAATAATTAATCTAGTAAGATGATCTACGTAAGAAAGTAAGTGTGATTAATCAATTAATGCT 120
QY 41 GlyGlyLysArgIleArgProValLeuLeuLeuThrLeuAspSerLeuAsnThrGlu 60
DB 121 GGAGGTAAACCAATCCGACCGACGATCTGTTATTACTCACTTAAGATTCACTAAATACCGAG 180
QY 61 TyrGluLeuGluMetLysSerValIleAlaLeuGluMetIleHisThrTyrSerLeuIle 80
DB 181 TATAGTATGAGTAAAGAAAGCGCAATTCACATAAATGATTCATCAATTAATCACTTAAT 240
QY 81 HisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHis 100
DB 241 CATATGACCTACACGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 300
QY 101 LysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120
DB 301 AAAGTAATGAGTGTGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 360
QY 121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGluArg 140
DB 361 GAACTTATTTCAAGTATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 420
QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSer 160
DB 421 CTGCAATAGCAAGTGTGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 480
QY 161 GluGlyGlnProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAla 180
DB 481 GAAGGCCAACCAATGATCTTGAAACTTTGAAATGATACAAACAAACAAACGAGGCA 540
QY 181 LeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrThrLys 200
DB 541 TTATTAATCTTTGCGGTTATGATGATGATTAATGATTAATGATTAATGATTAATGATTAAT 600
|||||
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QY 201 GluHisLeuGluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLeuValAspAspLeu 220  
 Db 601 GAACATTTAGAAATTAGTATCATTTAGTATGATGTTCCAGATTAAGATGATTTA 660  
 QY 221 LeuAspCysTyrGlyAspGluAlaLeuGlyLysLysValGlySerAspLeuGluAsn 240  
 Db 661 TTACACTGCTATGCTGATGAAGCAAGTATAGTAAAAAGGCGACGACTTGAATAAT 720  
 QY 241 AsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAlaGlyAspLysLeuThrTyr 260  
 Db 721 AATAAAGTAGCTGCGAGATTATAGGAAAGATGCGCAGAGATTAATTGACTTAT 780  
 QY 261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280  
 Db 781 CATAGAGCGCAGCAGTGATGAACCTAACGCAATTGATGACACTTCATACAAAACAC 840  
 QY 281 LeuLeuGluIleValAspLeu 287  
 Db 841 TTATTAGAAATCGTTGATTTA 861

## RESULT 3

US-08-781-986A-155/c  
 ; Sequence 155, Application US/08781986A  
 ; Publication No. US2003005436A1

## GENERAL INFORMATION:

APPLICANT: Charles Kunsch  
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
 NUMBER OF SEQUENCES: 5255  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248BP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 155:

SEQUENCE CHARACTERISTICS:

LENGTH: 1893 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-781-986A-155

## Alignment Scores:

Score: 2,12e-161 Length: 1893  
 Percent Similarity: 100.00% Matches: 287  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-09-925-637-64 (1-287) x US-08-781-986A-155 (1-1893)

QY 1 MetThrAsnLeuPheMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20  
 Db 1314 ATGACGAATCTACCCATGGAATTAATTAAGTGAAGTCAATTAAGATTAATCGGTGGC 1255  
 QY 21 IleAsnLysSerValMetAspThrGlnLeuGluGlnSerMetLeuTyrSerLeuAsnAla 40  
 Db 1254 AATTAATTAATCGATATGATATCTACGCTAGAAAGATGTTGATTCATTAATGCT 1195  
 QY 41 GlyGlyLysArgLysArgProValLeuLeuLeuThrLeuAspSerLeuAsnThrGlu 60  
 Db 1194 GAGGTTAAACGATCGACGACGACTCTGTTATTACCTGTTGATTCCTAATATCCGAG 1135  
 QY 61 TyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIle 80  
 Db 1134 TATGAGTTAGTATGATAGAGCCCAATGCGACATGAAGATTCATACATTCACCTTAT 1075  
 QY 81 HisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHis 100  
 Db 1074 CATGATGACCTTCCAGCGATGATTAATGATGATTCACGAGCAAAATTAACAATCAT 1015  
 QY 101 LysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120  
 Db 1014 AAAGTATATGATGAGTGGAGCTCGCATATTAAGCAGGTGATGCTTTATTACTAAACATT 955  
 QY 121 GluLeuLysSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg 140  
 Db 954 GAACCTTATTCAGATGATGATGATGATTAAGTATGATGAAGTAAATTAAGTTCTACACGG 895  
 QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSer 160  
 Db 894 CTGTCAATGCAAGATGTCATGTTGAAATGTCGCGCGTCAATGTATGATATGCAAAAC 835  
 QY 161 GluGlyGlnProIleAspLeuThrLeuGluMetIleHisLysThrLysArgAla 180  
 Db 834 GAAGGCCAACCAATGATCTTGAACCTTGAAGATGACACAAACAAACAAACAGAGCA 775  
 QY 181 LeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrThrLys 200  
 Db 774 TTATTACTTTTGGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715  
 QY 201 GluHisLeuGluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspLeu 220  
 Db 714 GAACATTTAGAAAGTATATGATATCATTTAGGATATGATTTCAAGATTAAAGATGATTTA 655  
 QY 221 LeuAspCysTyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGluAsn 240  
 Db 654 TTAGACTGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595  
 QY 241 AsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyr 260  
 Db 594 AATTAAGTACCTACGTCGTTATTAAGGAAAGTGGCGCAAGATTAATTTGACTTAT 535  
 QY 261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280  
 Db 534 CATAGAGCGCAGCAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475  
 QY 281 LeuLeuGluIleValAspLeu 287  
 Db 474 TTATTAGAAATCGTTGATTTA 454

## RESULT 4

US-10-329-624-155/c  
 ; Sequence 155, Application US/10329624  
 ; Publication No. US20040043037A1

## GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329, 624
FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956, 171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009, 861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781, 986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 1893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 155:
US-10-329-624-155

Alignment Scores:
Pred. No.: 2,12e-161 Length: 1893
Score: 1453.00 Matches: 287
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-925-637-64 (1-287) x US-10-329-624-155 (1-1893)

QY 1 MethrasleupPrometAenlyLeuileaspGluValasngluLeuSerValala 20
DB 1314 ATGACGATCTACCGAATGAATTAATGATGATGATGATGATGATGATGATG 1255
QY 21 IleaenlySerValMetaspThngluLeugluSerMetleuTySerleuaenla 40
DB 1254 ATAATTAATCAGTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1195
QY 41 GlygllySargileatgProvalleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 1194 GGAAGTAACGCAATCCGACGATCTGTTATTACTCTCTTAATTAATTAATCC 1135
QY 61 TygluLeuglyMetlySerVallealeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 1134 TATAGTACGTATGAAGAGCGCAATGCACTAGAAATGATTCATACATTAATCA 1075
QY 81 HisapaspLeuproalaMetaspasaspPyrargarggllyLeuLeuThraenhs 100
DB 1074 CATGTAGCTTACGACGATGATGATGATGATGATGATGATGATGATGATGAT 1015
QY 101 LysValTyrglyGluTyrThrAlaileuValaglyaspAlaLeuLeuThryala 120
DB 1014 AAAGTAATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 955
QY 121 GluLeuileSerSeraspaspargLeuThraspGluVallystleuValleuGlnarg 140

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/282, 122A
FILING DATE: 2003-02-20

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/253, 625
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/257, 931
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/267, 636
FILING DATE: 2000-12-22

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282, 122A
PRIOR APPLICATION NUMBER: 60/151, 078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267, 636

DB 954 GAACCTATTTCAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 895
QY 141 LeuSerlleaIaSerGlyHlsValGlyMetValGlyGlnMetLeuaspMetGlnSer 160
DB 894 CTGTCAATAGCAAGGTGCATGTTGGAATGTCGGCGGTCAAAATGATGATGATGATG 835
QY 161 GlnGlyGlnProIleaspLeuGluThrLeuGlnMetlleHlsTyThrlyThrGlyAla 180
DB 834 GAAAGCCACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 775
QY 181 LeuLeuThrPheAlaValMetSerlleAlaaspIleAlaenValaspThrThrly 200
DB 774 TTATTTAATCTTTGGGGTATGATGATGATGATGATGATGATGATGATGATGAT 715
QY 201 GlnHlsLeuGluSerTySerTyHlsleuGlyMetMetPheGlnlleLeuaspLeu 220
DB 714 GAACCTTTAGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 655
QY 221 LeuaspCyTyrglyaspGluAlaIySerleuGlyTylyValGlySeraspLeuGln 240
DB 654 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595
QY 241 AsnlySerThrTyTyValSerleuLeuGlyTyaspGlyAlaGluaspLeuThry 260
DB 594 AATTAATAGTACGTACGTAGTTTATTAGGAAAGATGCGCGAAGATTAATTAAT 535
QY 261 HisargaspAlaAlaValaspGluLeuThnglnleaspGlnPheasThrlyHls 280
DB 534 CATAGACGACGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
QY 281 LeuLeuGlnlleValaspLeu 287
DB 474 TTATTAGAAATCGTTGATTTA 454

RESULT 5
US-10-282-122A-8179
Sequence 8179, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zerkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyeth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282, 122A
PRIOR APPLICATION NUMBER: 60/151, 078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267, 636
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/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PAM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8179
/ LENGTH: 882
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-282-122A-8179

Alignment Scores:
Pred. No.: 8,02e-161 Length: 882
Score: 1444.00 Matches: 285
Percent Similarity: 99.65% Conservative: 1
Best Local Similarity: 99.30% Mismatches: 1
Query Match: 99.38% Indels: 0
DB: 13 Gaps: 0

US-09-925-637-64 (1-287) x US-10-282-122A-8179 (1-882)

QY 1 MetThAsnLeuProMetAsnLysLeuLeaSpGluValAsnAsnGluLeuSerValAla 20
DB 1 ATGACGAATCTTCCGATGCAATTAATTAATGATGAAGTCAATATGATATTCGGTTGCG 60

QY 21 IleAsnLysSerValMetAspThrGluLeuGluGluSerMetLeuTySerLeuAsnAla 40
DB 61 ATAAATAATTCAGTAATGATGATCTCAGCTAGAAAGAAAGCATGTTGATTCATTAATCT 120

QY 41 GlyGlyLysArgIleArgProValLeuLeuLeuLeuThLeuAspSerLeuAsnThrGlu 60
DB 121 GGAAGTAACGCATCCGACCACTTCTGTATTCTCATTGCTTACCTAATATCCGAG 180

QY 61 TyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTySerLeuIle 80
DB 181 TATGAGTATGAGTGTGAAGCGCAATTCAGTAAATATTCATATCATATTCACCTTAT 240

QY 81 HisAspAspLeuProIleMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHis 100
DB 241 CATGATGACCTACCGACGATGATATGATGATTCGACGAGGAAATTAACAATATAT 300

QY 101 LysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120
DB 301 AAGATTAATGATGAGTGAAGTGCATGATTAAGCAAGTGAAGCTTTTAACTTAACAT 360

QY 121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg 140
DB 361 GAACCTAATTCAGATGATATGATTAAGTGAAGTAAATTAAGTTCTTACACGAG 420

QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGluMetLeuAspMetGlnSer 160
DB 421 CTGTCAATAGCAAGTGTGATGATGGAATGCTCGCGGCTCAATGTTGATATGCAAGC 480

QY 161 GluGlyGlnProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAla 180
DB 481 GAAGGCAACCAATGATCTTGAACCTTGAAGAAAGATGACAAAACAAAACAGACACA 540

QY 181 LeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrThrLys 200
DB 541 TATTTAACCTTTGCGGTTATGAGTGCAGAGTATCGCTTAATGATGATGATCACTTAA 600

QY 201 GluHisLeuGluSerTySerTyHisLeuGlyMetMetPheGlnIleLysAspAspLeu 220
DB 601 GAACATTATGAAGAATATGATTAATCATTTAGTATGATGATGCTCCAGATTAAAGATAT 660

QY 221 LeuAspCysTyrGlyAspGluAlaLysLeuGlyLysLysValGlySerAspLeuGlnSer 240
DB 661 TTAGACTGCTATGAGTATGATGACAAAGTATGATGATGATGATGATGATGATGATGAT 720

QY 241 AsnLysSerThrTyValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyr 260
DB 721 AATTAATAAGTACGATGATGATTTATTTAGGAAAGATGCGGACAGAGATTAATGATCTAT 780
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QY 261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
DB 781 CATGACCAACCGACGAGTGAATGATTAATGATGATGATGATGATGATGATGATGATGAT 840

QY 281 LeuLeuGluIleValAspLeu 287
DB 841 TTATTAGAAATCGTTGATTTA 861

RESULT 6
US-09-815-242-8485
/ Sequence 8485, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlson, Karl L.
/ APPLICANT: Zykkind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8485
LENGTH: 882
TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(882)
US-09-815-242-8485

Alignment Scores:
Pred. No.: 1.38e-160 Length: 882
Score: 1442.00 Matches: 285
Percent Similarity: 99.30% Conservative: 0
Best Local Similarity: 99.30% Mismatches: 2
Query Match: 99.24% Indels: 0
DB: 9 Gaps: 0

US-09-925-637-64 (1-287) x US-09-815-242-8485 (1-882)

QY 1 MetThAsnLeuProMetAsnLysLeuLeaSpGluValAsnAsnGluLeuSerValAla 20
DB 1 ATGACGAATCTTCCGATGCAATTAATTAATGATGAAGTCAATATGATATTCGGTTGCG 60

QY 21 IleAsnLysSerValMetAspThrGluLeuGluGluSerMetLeuTySerLeuAsnAla 40
DB 61 ATAAATAATTCAGTAATGATGATCTCAGCTAGAAAGAAAGCATGTTGATTCATTAATCT 120

QY 41 GlyGlyLysArgIleArgProValLeuLeuLeuLeuThLeuAspSerLeuAsnThrGlu 60
DB 121 GGAAGTAACGCATCCGACCACTTCTGTATTCTCATTGCTTACCTAATATCCGAG 180
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QY	6	ThyGluuGluYwctLySerAlaIleAluGluMetIleHisThrYrSerLeuIle	80
Db	181	TATGAGTTCAGTATGCAAGCCGAATTCAGTAAGTAATTCATCATATTCATT	240
QY	81	HisAspSerLeuProAlaMetAspAsnaAspTYrAIGrGlyLysLeuThrAsnHis	1000
Db	241	CATGATGACCTTACGAGGATGATTAATGATGATTTACAGCAGGGAAATTACAAATCAT	3000
QY	101	LysValTYrGlyGluThrPhrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe	1200
Db	301	AAATATATATGTAAGTGAAGCTGCATATTAAGCAGGTAGCTTATTAATCAAAAGCAATTT	3600
QY	121	GluLeuLeuSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg	1400
Db	361	GAACTTATTTCAAGTGTGATGATTAATCACTGTAAGTAAATAAATTAAGCTTCAGACGG	4200
QY	141	LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSer	1600
Db	421	CTGTCATATACCAAGTGGTCATGTTGCAAAAGTCGGCGGTCAAAAGTTTGAAATGCCAAAGC	4800
QY	161	GluGlyGlnProIleAspLeuGluThrLysGluMetIleHisLysThrLysThrGlyAla	1800
Db	481	GAAAGCCAAACCAATTGATCTTGAAACTTTGAAAAGATACACAAAACAAAACAGAGCA	5400
QY	181	LeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrLys	2000
Db	541	CTATTTAACATTTCCGGTTATGAGTCAGACAGATACCGCTAATGTCAGATGCAACTAAA	6000
QY	201	GluHisLeuGluSerTYrSerTYrHisLysGlyMetMetPheGlnIleLysAspAspLeu	2200
Db	601	GAACTTTAGAAAGTTCATGATTCATCTTTAGGTATGAGTTCACATTAAGATGATTA	6600
QY	221	LeuAspCysTYrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGluAsn	2400
Db	661	TTAGACTGCTATGCTGATGACGCAAGTTAGCTAAAAAAGGCGACGACGATCTTGAAAT	7200
QY	241	AsnLysSerThrTYrValSerLeuGluGlyLysAspGlyAlaGluAspLysLeuThrTYr	2600
Db	721	AATTAAGATCAACGAGTTTATTAAGAAAGAGGGCGCGAAGATTAATTAATTAAT	7800
QY	261	HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis	2800
Db	781	CATGAGACCGACAGTGAATGAACCTAATGCAAAATGATGAACCAATTCATATACAAAACAC	8400
QY	281	LeuLeuGluIleValAspLeu 287	
Db	841	TTATTAGAAATCGTTGATTTA 861	

RESULT 7  
 US-09-815-242-4164  
 Sequence 4184, Application US/09815242  
 Patent No. US20020061569A1  
 GENERAL INFORMATION:  
 APPLICANT: Haselebeck, Robert  
 APPLICANT: Ohlsen, Karl L.  
 APPLICANT: Zyckind, Judith W.  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John D.  
 APPLICANT: Carr, Grant J.  
 APPLICANT: Yamamoto, Robert T.  
 APPLICANT: Xu, H. Howard  
 TITLE OF INVENTION: Identification of Bess  
 TITLE OF INVENTION: Prokaryotes  
 FILE REFERENCE: ELITRA.011A  
 CURRENT APPLICATION NUMBER: US/09/815,242  
 CURRENT FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26

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? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 4184
? LENGTH: 864
? TYPE: DNA
? ORGANISM: Staphylococcus aureus
US-09-815-242-4184

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Alignment Scores:		
Pred. No.:	2,09e-157	8
Score:	1415.00	215
Percent Similarity:	99.92%	Conservative: 0
Best Local Similarity:	99.92%	WtSimatches: 2
Query Match:	97.38%	Indels: 0
DB:	9	Gaps: 0

QY	MetAspIuLeuIleAspGluValAsnGluLeuSerValAlaIleAsnIysSerVal	25
Db	1 ATGAAATTAATTAATAGATCAAGTCAATATGATTAATTCGGTGGCAATTAATCACTGA	60
QY	26 MetAspThrGluLeuGluGlnSerMetLeuTyrserLeuAsnIleGlyValArgIle	45
Db	61 ATGGAATACCAAGCTGAGAAAGATGTTGTATTCATTAATAAGCTGGAGGAAACGGAT	120
QY	46 ArgProValIleuLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrsGluLeuGlyMet	65
Db	121 CGACCAAGTTCTGTATTACTACCTTAATTCATTAATTCACCAATTCAGATTGAGTTAGGATG	180
QY	66 LysSerAlaIleAlaLeuGluMetIleHisThrTyrserLeuIleHisAspAspLeuPro	85
Db	181 AAGAGGCAATTGCACCTAGAAATGATCATACATTCATTACTTATTCAGTAGCACTACCA	240
QY	86 AlaMetAspAsnAspAspPyrArgArgGlyLysIleuThrAsnHisIleValIleTyrsGlu	105
Db	241 GCGATGGAATAGATGATATGATTCGAGAGGAAATTAACAAATCTAAAGATATAGTGAG	300
QY	106 TrpThrAlaIleuLeuIleGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSerSer	135
Db	301 TGGACCTGCATATTACGAGGTGATGCTTTATTAACTAAAGCATTTGAACCTTATTCAAGT	360
QY	126 AspAspArgLeuThrAspGluValIleLysIleuValLeuGlnArgLeuSerIleAlaSer	145
Db	361 GATGATAGATTAACTGATGATGAAATTAATAAAGTTCTACACCGCTGCAATAGCAAGT	420
QY	146 GlyHisValGlyMetValGlyValIleMetLeuAspMetGlnSerGluGlyGlnProIle	165
Db	421 GGTCAAGTTGGAAATGGTGGCGCGTAAAGTATGATGACCAACGAGGCGCAACCAATT	480
QY	166 AspLeuGluThrLeuGluMetIleHisIleTyrsThrIleGlyAlaLeuLeuThrPheAla	185
Db	481 GACTTTGAAACCTTTGGAAATGATGATACAAAACAAAACAGAGACACTTATTACATTTCG	540
QY	186 ValMetSerSerAlaAspIleAlaAsnValAspAspThrThrIleGluHisIleGluSer	205
Db	541 GTTATAGTGACACAAATATCGCTAATGTCGATGATGCAATTAAGAAGCACTTTGAAAGT	600
QY	206 TyrSerTyrsIleLeuGlyMetMetPheGlnIleLysAspAspLeuLeuAspCysTyrsGly	225
Db	601 TATAGTTATCATTTAGGTATGATGATGTTTCAGATTAAAGATGATTTATTAGACTGCTAGGT	660
QY	226 AspGluAlaIleLeuGluGlyLysValGlyLysSerAspLeuGluAsnAsnLysSerThrTyr	245
Db	661 GATGAAGCGAAAGTTAGTATAAAAAGTGGCGCGCATCTTGAAATATATTAAGATCACTAC	720

QY 246 ValSerLeuLeuGlyIlysaSpGlyValaGluAspLysLeuThrTyRHisArgAspAlaIala 265  
Db 721 GGGAGTTTATTAGGAAAAAGATGCGCAGAAAGATAAATTACCTTATCATGAGACCGCAGCA 780  
QY 266 ValAspGluLeuThrGlnIleAspGluGlnIlePheAsnThrLysHisLeuLeuGluIleVal 285  
Db 781 GTGGATGAACCTAATGCAAAATTGATGAACCAATTCATACAAACACTTATTAGAAATCGTT 840  
QY 286 AspLeu 287  
Db 841 GATTTA 846  
RESULT 8  
US-10-282-122A-35068  
Sequence 35068, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zykkind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 35068  
LENGTH: 879  
TYPE: DNA  
ORGANISM: Staphylococcus haemolyticus  
US-10-282-122A-35068  
Alignment Scores:  
Pred. No.: 4,64e-113 Length: 879  
Score: 1040.00 Matches: 18  
Percent Similarity: 83.62% Conservative: 42  
Best Local Similarity: 68.99% Mismatches: 47  
Query Match: 71.58% Indels: 0  
DB: 13 Gaps: 0  
US-09-925-637-64 (1-287) X US-10-282-122A-35068 (1-879)

QY 1 MetThrAsnLeuProMetAsnLysLeuIleAspGluValAsnGluLeuSerValAla 20  
Db 1 ATGGCAAAAGAAAGTCAAAAGAAATGAATTATTAATCAAAATTAATAGCGCTTTCAGCGTGTA 60  
QY 11LeAsnLysSerValMetAspThrGlnLeuGluGlnIleSerMetLeuTyRSerLeuAsnAla 40  
Db 61 ATCGAAACTTCACACCACTTAATACCAATCTTGAGAAAGATTCGCAATTTCTTCGAATGCG 120  
QY 41 GlyIlysaArgIleArgProValLeuLeuLeuLeuLeuAspSerLeuAsnThrGlu 60  
Db 121 GTGTGTAAGAAATPAGAACCACTTCTGTATTTTAAACATAGATGATTAATCAAGAT 180  
QY 61 TyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetLeuIleThrTyRSerLeuIle 80  
Db 181 TATTAAGAAAGTAAAAAAAGTCACTTCGCTTGGAAATGATTCACACGTATTTCTTAATT 240  
QY 81 HisAspAspLeuProAlaMetAspAsnAspAspTyRArgArgGlyLysLeuThrAsnHis 100  
Db 241 CATGATGATCTTCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
QY 101 LysValTyRArgIlyGluThrPheAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120  
Db 301 AAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
QY 121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg 140  
Db 361 GAATCATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSer 160  
Db 421 TTACCGCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
QY 161 GluIlyGlnProIleAspLeuGluThrLeuGluMetLeuIleHisTyRThrLysGlyAla 180  
Db 481 GAAATTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
QY 181 LeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLys 200  
Db 541 TTACTTCATTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
QY 201 GluHisLeuGluSerTyRSerTyRHisLeuGluMetLysPheGlnIleLysAspAspLeu 220  
Db 601 CAAAGCTTTAAAGATTTTAATCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
QY 221 LeuAspCysTyRArgIlyAspGluAlaLysLeuGlyLysLysValGlySerAspLeuGluAsn 240  
Db 661 CTCGACGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
QY 241 AsnLysSerThrTyRValSerLeuLeuGlyLysAspGlyValaGluAspLysLeuThrTyR 260  
Db 721 CACAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
QY 261 HisArgAspAlaAlaValaLeuAspGluLeuThrGlnIleAspGluGlnIlePheAsnThrLys 280  
Db 781 CATTAAGATGCTGCAAAAATCAATGAACAACTTCTTCACACATGATGATTAATTAACCT 840  
QY 281 LeuLeuGluIleValaAspLeu 287  
Db 841 CTATTAGATATCGTTGAGCTT 861  
RESULT 9  
US-10-282-122A-34531  
Sequence 34531, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zykkind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John



```

APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 34531
LENGTH: 879
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-10-282-122A-34531

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Alignment Scores:
Pred. No.: 4,19e-110      Length: 879
Score: 1015.00           Matches: 197
Percent Similarity: 82.93% Conservative: 41
Best Local Similarity: 68.64% Mismatches: 49
Query Match: 69.86%      Indels: 0
DB: 13                   Gaps: 0

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US-09-925-637-64 (1-287) x US-10-282-122A-34531 (1-879)

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QY 1 MetThrAsnLeuProMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
DB 1 ATGAAGAAGACTACAGATGAAATTAATTAATAATTAATTAATACATCAGCAATTAAGTCA 60
QY 21 IleAsnLysSerValMetAspThrGlnLeuGluGluSerMetLeuTyrSerLeuAsnAla 40
DB 61 ATACATCATCATCATTAAATTAATTAAGAAAGATGAAATTAATTAATTAATTAATTAAT 120
QY 41 GlyGlyLysArgIleArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGlu 60
DB 121 GGTGTAAAGAAATACAGCAATGATATTAATTAATTAATTAATTAATTAATTAATTAAT 180
QY 61 TyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIle 80
DB 181 TATCAACAAGACTAAATATGCTTTAGCATTTGAAATGATTCATCTTATCTTTAATT 240
QY 81 HisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHis 100
DB 241 CATGATGATTTACCGCAATGATGATATACATTAACCTTAAGCAAAATTAACAATCAT 300
QY 101 LysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120
DB 301 AAAGTTTATGTGATGAAAGCCATCTCTGCTGTGATGATTAATTAACCAAAAGCTTTT 360
QY 121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGluArg 140

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DB 361 GAATTAAGTTTCATATGATACATACATTAAGATAGTGGAAAGTAAATTAATAAAGA 420
QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSer 160
DB 421 CTTTCAAAAGCAAGGACATTTGGGAATGGTGGTGGCCAAAGCGCTGATATGAAAGT 480
QY 161 GlyGlyGlnProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAla 180
DB 481 GAAAGGAAGTCAATTCGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
QY 181 LeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrLys 200
DB 541 TTACTAAATTTTTCAGTATGCTGCGGTAAACATTTGTCAGATGAAGCAAAATATTGCT 600
QY 201 GluHisLeuGluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeu 220
DB 601 AAGAAATTAAGATGAAATTTAGTCATCATTTTAGAATGATGCTTTCAAAATTAAGATTA 660
QY 221 LeuAspCysTyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGluAsn 240
DB 661 CTGATGCTATGATGATGATGATCAAACTGCAAAAAAGTAGGCAAGATATTAATAAT 720
QY 241 AsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyValGluAspLysLeuThrTyr 260
DB 721 CATAAAGACTATTAATGTTCTTTACTTGAAAAGAGAGAGAGAGAAAGTTTAACAAT 780
QY 261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
DB 781 CATCAATATCTGCTATGACATGCTTAATCAATTTCTGATCATATATGATATCTTCTGA 840
QY 281 LeuLeuGluIleValAspLeu 287
DB 841 TTAAGTATGATTTGATGATTTA 861

RESULT 10
US-10-282-122A-24756
Sequence 24756, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09

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; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PAM
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24756
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Listeria monocytogenes
; IS-10-282-122A-24756

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Alignment Scores:	
Pred. No.:	3,73e-73
Score:	707.50
Percent Similarity:	69.29%
Best Local Similarity:	52.86%
Query Match:	48.35%
DB:	13
Length:	8
Matches:	1
Conservative:	2
Mismatches:	6
Indels:	2
Gaps:	2

US-09-925-637-64 (1-287) x US-10-282-122A-24756 (1-882)

[illegible]

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Oy      268 G|UleuThrGlnIleAspGluGlnPheAsnThrLysHisIeuLeuCluIleValAspLeu 287
          ||::: || |::: :: |||||::: |||||
Db      808 GCCGTTTCAGGGCATGAT-----TTCGATGATGAATTCTTGAAACTGTGCTGATTTA 861
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RESULT 11  
US-10-398-221-3823  
; Sequence 3823, Application US/10398221  
; Publication No. US20040018114A1  
; GENERAL INFORMATION:  
; APPLICANT: KUNST, Frederik  
; APPLICANT: GAASER, Philippe  
; TITLE OF INVENTION: Listeria innocua, genome and applications

Alignment Scores:	
pred. No.:	3 79e-71
Score:	695.50
Percent Similarity:	68.93%
Best Local Similarity:	52.86%
Query Match:	47.87%
DB:	16
length:	5635
Matches:	148
Conservative:	45
Mismatches:	82
Indels:	
Gaps:	2

US-09-925-637-64 (1-287) X US-10-398-221-3823 (1-5635)

OY		8	LysLeuIleAspGluValaAsnAsnGluLeuSerValAlaIleAsnLysSerValMetSer	27
Dd		2914	AAATGTATTGATGG-----TCGCTTTTAAAGAAATAACCGAGCAATATCCAA	296
OY		28	ThrGlnLeuGluGlnSerMetLeuTySerSerLeuAsnIagiGlyLysArgIIeAPro	47
Dd		2965	CCTAGATTTAAAGAAGTCCATGTTATATTCGTTCAACAAGGTGA AAAACGAGATTCGTC	3024
OY		48	ValIleuLeuLeuLeuthrIleAspSerLeuAsnThrcIuTyrgIuLeuGIyMetLysSer	67
Dd		3025	ATGCTAATTTTTTGCTACACTTCACGCCTTAAGATAATCCGCTTTAAGGTGTA AACA	3084
OY		68	AlaIleIleLeuGluMetIleHisThrTySerLeuIleHisAspAspLeuProAlaMet	87
Dd		3085	GCAACGCCGCTTAGAAAGATTCATCCTATACGCTATACCATGATGATTTACCGACGATG	3144
OY		88	AspAsnAspAspPyrraIgaTrgGlyLysLeuThraSnhIslyValITyrGIyGluTrpThr	107
Dd		3145	GATATATATATACATTCGTCGCGGCAATATATCATATAAAGTTTTGGGGAATCACT	3204
OY		108	AlaIleLeuIagiAspAlaLeuLeuThrcLyAlaPheGluLeuIleSerSerAspAsp	127
Dd		3205	GCGATTTTGGCAGAGACGCTTACTAACGCTTCCTTTTCTATTTTAGCGGACGACGA	3264
OY		128	ArgIeuThraspGluValLysIleLysValIleuGlnArgLeuSerIIeAlaSerGIyHis	147
Dd		3265	AATTTATCTTTTGGAAACACCATATGCTTTGATTATCAAAATTGTTTTAGTAGTGGTCA	3324
OY		148	ValGIyMetValGIyGIyGlnMetLeuAspMetGlnSerGIyGluGlnProIIeAspLeu	167
Dd		3325	GAAGGAATGTGTGGCGGTCACTTCGACATATGTGAGCGACGAAAACAACAAGTACATTA	3384

QY 168 GluThrleuGluMetIleHisIysThrThrGlyAlaLeuLeuThrPheAlaValMet 187  
DB 3385 GAAGAACTATCATCCATCCATGACGAGAAACAGGCAATATTATTTTGGCGTAAC 3444  
QY 188 SerAlaIleAspIleAlaAsnValAspAspThrThrIleGluHisIleuGluSerIysSer 207  
DB 3445 TCTGCTCGCAAAATGACAGAAAGCTGACCCGGAACAAAGAAAGATTACGATTTTGGG 3504  
QY 208 TyrHisIleuGluMetMetPheGlnIleIleAspAspLeuLeuAspCysTyrGlyAspGlu 227  
DB 3505 GAAATATTTGGAGATTGATTCGCAATACGACGACATATTTTGAATGTTATTTGGTGA 3564  
QY 228 AlaIleuGluGlyIleValIleGlySerAspLeuGluHisIleuGluSerIysSer 247  
DB 3565 ACAGAAATGGGTAAAGACAGGGGTGACGCTTTCTGAAACAAAGTACCTATCCCGGA 3624  
QY 248 LeuLeuGlyIleAspGlyAlaGluAspIleuThrTyrHisArgAspAlaAlaValAsp 267  
DB 3625 TTACTCAGCTTGATGGTCCAAAGGCAATTAATGAGCATGTTGCGATTGCAAAAGTCA 3684  
QY 268 GluLeuThrGlnIleAspGluGlnPheAsnThrIleHisIleuGluIleValAspGlu 287  
DB 3685 GCGCTTCAGGCGCATGAT-----TTTGATGATGAAATTTCTTGAACCTTGCTGATTTA 3738

## RESULT 12

US-09-815-242-2822/C  
Sequence 2822, Application US/09815242  
Parent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 2822  
LENGTH: 413  
TYPE: DNA  
ORGANISM: *Staphylococcus aureus*  
US-09-815-242-2822

Alignment Scores:  
Pred. No.: 3,698-72 Length: 413  
Score: 690.00 Matches: 137  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 47.49% Indels: 0  
DB: 9 Gaps: 0

US-09-925-637-64 (1-287) x US-09-815-242-2822 (1-413)

QY 54 LeuAspSerIleuAsnThrGluTyrGluLeuGlyMetIleSerAlaIleAlaLeuGluMet 73  
DB 413 TTGATTTACTTAATATCCAGATATGATTTAGTATGAAAGCGCATTTGCTGAAATG 354  
QY 74 IleHisThrTyrSerIleuIleHisAspAspLeuPheAlaMetAspAsnAspTyrArg 93  
DB 353 ATTCAATACATATTCATCTTATTCATGATGACCTACAGCGATGATTAATGATGATATGCA 294  
QY 94 ArgGlyIleValLeuThrAsnHisIleValTyrGlyGluTyrPheAlaIleLeuAlaGlyAsp 113  
DB 293 CGAGGAAATTAATTAACAAATCAATTAATATGATGATGATGATGATGATGATGAT 234  
QY 114 AlaLeuLeuThrIleValAlaPheGluLeuIleSerSerAspAspArgLeuThrAspGluVal 133  
DB 233 GCTTTATTAATTAAGCATTTGAACTTATTTCAAGTATGATGATTAATGATGATGATGAT 174  
QY 134 LysIleIleValLeuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGly 153  
DB 173 AAAATTAAGTTCTACCAACGCTGTCAATACCAAGTGTCAATGTGATGATGATGATGAT 114  
QY 154 GlnMetLeuAspMetGlnSerGluGlyGlnPheIleAspLeuGluThrLeuGluMetIle 173  
DB 113 CAAATGTTAGATATGCAAGGAGGCAACCAATGATCTTGAACCTTGGAAATGATA 54  
QY 174 HisIleThrIleThrGlyAlaLeuLeuThrPheAlaValMetSerAlaAla 190  
DB 53 CACAAACAAACAAACAGGAGCATTAATTAATTTTGGGTTATGATGATGATGATGATGAT 3

## RESULT 13

US-10-282-122A-5390/C  
Sequence 5390, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Lianggu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forey, R.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PAM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 5390  
/ LENGTH: 413  
/ TYPE: DNA  
/ ORGANISM: Staphylococcus aureus  
US-10-282-122A-5390

## Alignment Scores:

Pred. No.: 3,696-72 Length: 413  
Score: 690.00 Matches: 137  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 47.49% Indels: 0  
DB: 13 Gaps: 0

US-09-925-637-64 (1-287) x US-10-282-122A-5390 (1-413)

QY 54 LeuApsSerLeuAenThrgLutrgLuleuGlyMeLysSerAlaLeuAlaLeuGluMet 73  
DB 413 TTAGATTCTCAATAACGAGATGAGTTAGGATGAGAGGCAATTGCACTGAAATG 354  
QY 74 LLeHSTrrTYrSerLeuLLeHsAspAspLeuProAlaMetAspAspAspTYrArg 93  
DB 353 ATTCTATACATATTCCTATTATCATGATGACCTACCGAGATGATATGATGATATTCGA 294  
QY 94 AsGGLyLysLeuThrAspHisLysValTYrGlyGluTPThrAlaLeuAlaGlyAsp 113  
DB 293 CGAGGAATTTACAAATCATATAAGTATATGCTGAGTGCATCTGCATATTAGCGAGTAT 234  
QY 114 AlaLeuLeuThrLysAlaPheGluLeuLLeSerSerAspAspArgLeuThrAspGluVal 133  
DB 233 GCTTATATTACAAAGCAATTGAACTTATTCATGATGATAGATTAACTGATGAGTA 174  
QY 134 LysLLeValLeuGluArgSerLeuLLeAspSerGlyHisValGlyMetValGly 153  
DB 173 AAAATTAAGTTCTCAAGGCTGTCAATAGCAAGTGGTCATGTGGATGGTGGCGGT 114  
QY 154 GlnMetLeuAspMeGlnSerGluGlyGlnProLLeAspLeuGluThrLeuGluMet 173  
DB 113 CAAATGTTAGATATCCAAAGCGAAGCCACCAATTGATCTTGAATGTA 54  
QY 174 HisLysThrLysThrgLysAlaLeuLeuThrPheAlaValMetSerAla 190  
DB 53 CCAAAACAAAACAGAGCAATTATTACTTTGGGTTATGAGTCAGCA 3

## RESULT 14

US-10-398-221-8/c  
/ Sequence 8, Application US/10398221  
/ Publication No. US20040018514A1  
/ GENERAL INFORMATION:  
/ APPLICANT: KUNST, Frederik  
/ APPLICANT: GLASER, Philippe  
/ TITLE OF INVENTION: Listeria innocua, genome and applications  
/ FILE REFERENCE: 344 702 - US  
/ CURRENT APPLICATION NUMBER: US/10/398,221  
/ PRIOR FILING DATE: 2003-03-27  
/ PRIOR APPLICATION NUMBER: PCT/FR 01/03 061  
/ PRIOR FILING DATE: 2001-10-04  
/ PRIOR APPLICATION NUMBER: FR 00/12 697  
/ PRIOR FILING DATE: 2000-10-04  
/ NUMBER OF SEQ ID NOS: 4025  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 8  
/ LENGTH: 495269  
/ TYPE: DNA  
/ ORGANISM: Listeria innocua  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ LOCATION: (1)..(end)  
/ OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u  
US-10-398-221-8

## Alignment Scores:

Pred. No.: 3,096-67 Length: 495269

Score: 686.50 Matches: 146  
Percent Similarity: 68.21% Conservative: 45  
Best Local Similarity: 52.14% Mismatches: 84  
Query Match: 47.25% Indels: 5  
DB: 16 Gaps: 2

US-09-925-637-64 (1-287) x US-10-398-221-8 (1-495269)

QY 8 LysLeuLLeAspGluValAsnGlnLeuSerValAlaLLeAsnLysSerValMetAsp 27  
DB 366194 AAAGTACTGATGAG-----TCGCTTTTAAAGAAATAAATATGCGCATATTCGA 366144  
QY 28 ThrGlnLeuGlnGlnSerMetLeuTYrSerLeuAsnAlaGlyValLysArgLLeAspPro 47  
DB 366143 CTTAAGTTGAAGAAATCAATGTTATTTATTCAGTCGAAGCTGGCGAAACGAATTCGTCCA 366084  
QY 48 ValLeuLeuLeuThrLeuAspSerLeuAsnThrgLutrgLuleuGlyMetLysSer 67  
DB 366083 ATGCTTGTTTTTCACACGCTTCAAGCCTTAATATATGACCAATGCGGTTTAAACCA 366024  
QY 68 AlaLLeAlaLeuGluMetLLeHSTrrTYrSerLeuLLeHsAspAspLeuProAlaMet 87  
DB 366023 GCTACGCACTTGAATGATGATCATATGATGACGTTAATTCACGATATTTACCGCAATG 365964  
QY 88 AspAsnAspAspTYrArgArgGlyLysLeuThrAsnHisLysValTYrGlyGluTPThr 107  
DB 365963 GATGATGATGATCTATTCGACCGCGGAATGAGCAACCAATTAATATACGATGCAACA 365904  
QY 108 AlaLLeValaGlyAspAlaLeuLeuThrLysAlaPheGluLeuLLeSerSerAspAsp 127  
DB 365903 GCAATTTTACCGAGAGATGCTTGTITTAACACTGCTTTTCTATTAGTGAAGATGA 365844  
QY 128 ArgLeuThrAspGluValLysLLeValLeuGluArgSerLeuLLeAspSerGlyHis 147  
DB 365844 AATCTATCTTTCGAAACGCGTATGCTTATTAATTAACAAATGTTATAGCATGAGCA 365784  
QY 148 ValGlyMetValGlyGlnMetLeuAspMeGlnSerGluGlyGlnProLLeAspLeu 167  
DB 365783 GAAGGATGAGTATGCTGGGCAACAGCCGATATGAAAGCTGAATAACAAAGTCACATTA 365724  
QY 168 GlnThrLeuGluMetLLeHSTrrTYrSerThrgLysAlaLeuLeuThrPheAlaValMet 187  
DB 365723 GAAGAAATTACCAATCCACGCTCGCAAACTGCGAATTAATTTTCGAGTAACC 365664  
QY 188 SerAlaAlaAspLLeAlaAsnValaAspThrThrLysGluHisLeuGlnSerTYrSer 207  
DB 365663 TCAGCGCAAAAATCGCTGAAGCAACTCCAGAACAAACAAAGATTACGAATTTTGGCA 365604  
QY 208 TyrHisLeuGlyMetLLePheGlnLLeLysAspAspLeuLLeAspTYrGlyAspGlu 227  
DB 365603 GAAATATTCGGATGCTGTTTCAAAATTAAGCAAGATATTTAATGATTAATTCGCGATGA 365544  
QY 228 AlaLysLeuGlyLysLysValaGlySerAspLeuGluAsnLysSerThrTYrValSer 247  
DB 365543 ACATAATGCTGTAATAAGACAGGCGTCGACCGTTCTGATATTAAGTACTATCCGGA 365484  
QY 248 LeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTYrHisArgAspAlaAlaValaAsp 267  
DB 365483 TTACTCACCTCGAAGGTGTAAACGGCAATTAAATGAGCATTTTCAATGGCAAGTCA 365424  
QY 268 GlnLeuThrgLlnLeuAspGlnLLePheAsnThrLysHisLeuGlnGluValaAspLeu 287  
DB 365423 GCGCTTCAAGACATGAT-----TTGACAGATGAATCTCTTAACTATGCTGATTTA 365370

## RESULT 15

US-10-398-221-2058  
/ Sequence 2058, Application US/10398221  
/ Publication No. US20040018514A1  
/ GENERAL INFORMATION:  
/ APPLICANT: KUNST, Frederik  
/ APPLICANT: GLASER, Philippe  
/ TITLE OF INVENTION: Listeria innocua, genome and applications  
/ FILE REFERENCE: 344 702 - US





TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US/09/134,001C  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3171  
LENGTH: 302  
TYPE: PR1  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3171

Query Match 69.9%; Score 1015; DB 4; Length 302;  
Best Local Similarity 68.6%; Pred. No. 6.5e-93;  
Matches 197; Conservative 41; Mismatches 49; Indels 0; Gaps 0;

QY 1 MTNLPNNKLTIDEVNNELSVAINKSVMDTLEESYVSLNAGKRIKIRPVLLLTLSINTS 60  
DB 10 MKKLQNNKLTINIINTSINKSIQSSPLKTNLEESWKYSLNAGKRIKIRPVLLLTLSINTS 69  
QY 61 YELGKSAIALEMHTHTSLIHDHDPANDNDYRGRKLTNNKVTGEWTAIIAGDALLTKAF 120  
DB 70 YQGLNSKALEMHTHTSLIHDHDPANDNDYRGRKLTNNKVTGEWTAIIAGDALLTKAF 129  
QY 121 ELISSDDLTDVETKYLORLSIASGHVGVGQMLDMOSEGQPIDLETLEMIHKTGTGA 180  
DB 130 ELVNDTTEBSVAVSIIRKLSKASGHLGVGQALDMESEKSIKLETLESHKTKTA 189  
QY 181 LITAVMSADIANAVDTTKEHLESYSYHGMFQIKODLLDCYGEBAKIGKVGSDLEN 240  
DB 190 LITAVMSADIANAVDTTKEHLESYSYHGMFQIKODLLDCYGEBAKIGKVGSDLEN 249  
QY 241 NKSTYVSLGKDGAEKLTTHRDAAVDELQIDQFNTKHLLEIVDL 287  
DB 250 HKSTYVSLGKDGAEKLTTHRDAAVDELQIDQFNTKHLLEIVDL 296

RESULT 3  
US-08-534-910B-9  
Sequence 9, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOYAMA, Taneoschi  
TITLE OF INVENTION: Mutated fatty acid synthase capable  
TITLE OF INVENTION: Of synthesizing geranylgeranyldiphosphate and gene coding therefor  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-0796  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-9

Query Match 45.2%; Score 657; DB 1; Length 297;  
Best Local Similarity 47.7%; Pred. No. 2.7e-57;  
Matches 133; Conservative 57; Mismatches 83; Indels 6; Gaps 2;

QY 1 MTNLPNNKLTIDEVNNELSVAINKSVMDTLEESYVSLNAGKRIKIRPVLLLTLSINTS 56  
DB 1 MAQSVQFNEQKQAVTALSRYIERLEGRAKIKKAAVSLNAGKRIKIRPVLLLTLSINTS 60  
QY 57 INTEYELGKSAIALEMHTHTSLIHDHDPANDNDYRGRKLTNNKVTGEWTAIIAGDALL 116  
DB 61 LGKDPAGVGPVACALEMHTHTSLIHDHDPANDNDYRGRKLTNNKVTGEWTAIIAGDALL 120  
QY 117 TPAFELIS--SDPRLTDEVKIKVLRSLIASGHVGVGQMLDMOSEGQPIDLETLEMIH 174  
DB 121 TPAFELITIDERLPPSVRLRLRLKKAQPSGVAGQALDMESEKSIKLETLESHKTKTA 180  
QY 175 KTKTGALLITAVMSADIANAVDTTKEHLESYSYHGMFQIKODLLDCYGEBAKIGKVG 234  
DB 181 RHKTGKMLQVSHAGALLGADARQTRLEDEFAALIGAFQIRDDILDEGAEEKIGKRV 240  
QY 235 GSDLENKSTYVSLGKDGAEKLTTHRDAAVDELQID 273  
DB 241 GSDQNNKATYFALLSLAGAEKLTTHLEAAQRRLNAD 279

RESULT 4  
US-08-886-466-2  
Sequence 2, Application US/08886466C  
Patent No. 6040165  
GENERAL INFORMATION:  
APPLICANT: Naita, Keisshi  
APPLICANT: Iehida, Chika  
APPLICANT: Takeuchi, Yoshie  
APPLICANT: Ohto, Chikara  
APPLICANT: Ohnuma, Shinichi  
APPLICANT: Mishiho, Tokuzo  
TITLE OF INVENTION: MUTANT PREANYL DIPHOSPHATE SYNTHASE  
FILE REFERENCE: 77670/494  
CURRENT APPLICATION NUMBER: US/08/886,466C  
CURRENT FILING DATE: 1997-07-10  
EARLIER APPLICATION NUMBER: JP 8-191635  
EARLIER FILING DATE: 1996-07-03  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 2  
LENGTH: 297  
TYPE: PR1  
ORGANISM: Bacillus stearothermophilus  
US-08-886-466-2

Query Match 45.0%; Score 654; DB 3; Length 297;  
Best Local Similarity 47.7%; Pred. No. 5.3e-57;  
Matches 133; Conservative 55; Mismatches 85; Indels 6; Gaps 2;

```

QY      1 MTNLPMNKLIDEVNNELSVAINKSVM---DTQLEESMLYSINAGGRIRPVLLLTLLDS 56
      1 MAOLSVGEFLNEKQAVETALSRVIERLGPAPKAKMAVSLGAGGRIRPVLSTVRA 60
QY      57 LNTVEYELGKMSALALEMIHTYSLIHDDLPMANDDYRSGKLTNNKXYGEMWAILAGDALL 116
      61 LGKDPVAVGIPVACALIMHTYSLIHDDLPSMNDDLRRCKPTNNKXVFGEMWAILAGDGLL 120
QY      117 TKAFELIS--SDRLTDEVYIKVLRSLASGHVGVGGMMDMOSGQPIDLETLEMTH 174
      121 TYAFQILTEIDDERIPPSVRLRIERLAKAAGPEGVAQADMEGEGKTLTISELEYIH 180
QY      175 KKTGALLTFVAVMSADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGBEAKLGKRV 234
      181 RHKTGKMLQYSVHAGAILGADARQTRLEDFAHGLAFQIRDDILDIGABEKIKGPV 240
QY      235 GSDLENKSTYVSLGKQGAEDKLTTHRDAVDELTOID 273
      241 GSDQSNKATYYPALLSLAGAKEXLAFHIEAQRHLRNAD 279

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# RESULT 5

```

US-09-475-304-2
; Sequence 2, Application US/09475304
; Patent No. 6225096
; GENERAL INFORMATION:
; APPLICANT: Narita, Keisshi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohts, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/09/475,304
; CURRENT FILING DATE: 1999-12-30
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-475-304-2

```

```

Query Match      45.0%; Score 654; DB 3; Length 297;
Best Local Similarity 47.7%; Pred. No. 5.3e-57;
Matches 133; Conservative 55; Mismatches 85; Indels 6; Gaps 2;

```

```

QY      1 MTNLPMNKLIDEVNNELSVAINKSVM---DTQLEESMLYSINAGGRIRPVLLLTLLDS 56
      1 MAOLSVGEFLNEKQAVETALSRVIERLGPAPKAKMAVSLGAGGRIRPVLSTVRA 60
QY      57 LNTVEYELGKMSALALEMIHTYSLIHDDLPMANDDYRSGKLTNNKXYGEMWAILAGDALL 116
      61 LGKDPVAVGIPVACALIMHTYSLIHDDLPSMNDDLRRCKPTNNKXVFGEMWAILAGDGLL 120
QY      117 TKAFELIS--SDRLTDEVYIKVLRSLASGHVGVGGMMDMOSGQPIDLETLEMTH 174
      121 TYAFQILTEIDDERIPPSVRLRIERLAKAAGPEGVAQADMEGEGKTLTISELEYIH 180
QY      175 KKTGALLTFVAVMSADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGBEAKLGKRV 234
      181 RHKTGKMLQYSVHAGAILGADARQTRLEDFAHGLAFQIRDDILDIGABEKIKGPV 240
QY      235 GSDLENKSTYVSLGKQGAEDKLTTHRDAVDELTOID 273
      241 GSDQSNKATYYPALLSLAGAKEXLAFHIEAQRHLRNAD 279

```

# RESULT 6

US-09-101-126-3

```

; Sequence 3, Application US/09101126
; Patent No. 6316216
; GENERAL INFORMATION:
; APPLICANT: OHTO, CHIKARA
; APPLICANT: NAKANE, HIROYUKI
; APPLICANT: NISHINO, TOKUZO
; APPLICANT: OHNUMA, SHINICHI
; APPLICANT: HIROOKA, KAZUTAKE
; TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES
; FILE REFERENCE: 77670/566
; CURRENT APPLICATION NUMBER: US/09/101,126
; CURRENT FILING DATE: 1999-04-27
; EARLIER APPLICATION NUMBER: PCT/JP97/03921
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: JP 8-307506
; EARLIER FILING DATE: 1996-11-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; OTHER INFORMATION: 86-92 is an Asp-rich domain
US-09-101-126-3

```

```

Query Match      45.0%; Score 654; DB 4; Length 297;
Best Local Similarity 47.7%; Pred. No. 5.3e-57;
Matches 133; Conservative 55; Mismatches 85; Indels 6; Gaps 2;

```

```

QY      1 MTNLPMNKLIDEVNNELSVAINKSVM---DTQLEESMLYSINAGGRIRPVLLLTLLDS 56
      1 MAOLSVGEFLNEKQAVETALSRVIERLGPAPKAKMAVSLGAGGRIRPVLSTVRA 60
QY      57 LNTVEYELGKMSALALEMIHTYSLIHDDLPMANDDYRSGKLTNNKXYGEMWAILAGDALL 116
      61 LGKDPVAVGIPVACALIMHTYSLIHDDLPSMNDDLRRCKPTNNKXVFGEMWAILAGDGLL 120
QY      117 TKAFELIS--SDRLTDEVYIKVLRSLASGHVGVGGMMDMOSGQPIDLETLEMTH 174
      121 TYAFQILTEIDDERIPPSVRLRIERLAKAAGPEGVAQADMEGEGKTLTISELEYIH 180
QY      175 KKTGALLTFVAVMSADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGBEAKLGKRV 234
      181 RHKTGKMLQYSVHAGAILGADARQTRLEDFAHGLAFQIRDDILDIGABEKIKGPV 240
QY      235 GSDLENKSTYVSLGKQGAEDKLTTHRDAVDELTOID 273
      241 GSDQSNKATYYPALLSLAGAKEXLAFHIEAQRHLRNAD 279

```

# RESULT 7

```

US-08-534-910B-7
; Sequence 7, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OHTA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyocho
; APPLICANT: KOYAMA, Taneoshi
; TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
; OF SYNTHESIZING GERANYLGERANYLDIPHOSPHATE AND GENE CODING THE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405

```



## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toftennet, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-7

Query Match 44.9%; Score 653; DB 1; Length 297;  
Best Local Similarity 47.3%; Pred. No. 6,76-57;  
Matches 132; Conservative 56; Mismatches 85; Indels 6; Gaps 2;

QY 1 MTNLPNKLIDEVNNELSVAINKSVM---DTOLEESMLYSLNAGGKRIPIVLLITLDS 56  
DB 1 MAQSVSEQFLNEQKQAVETALSRYIERLEGPAKVKKMAVSLKGGKRIPIVLLITLSTVQA 60  
QY 57 INTEVEYELGKSAIALEMHTYSLIHDDLPAVNDYRSGKLTNNKYGGWTAILAGDALL 116  
DB 61 LGKDPVAGLPVACALIEHTYSLIHDDLPSMNDLDRGKPTNNKYGGWTAILAGDALL 120  
QY 117 TKAFELIS--SDRLTDEVKIKVLRSLASGHVGMVGGQMLDMQSEGPIDLETLEMTH 174  
DB 121 TYAFQILTEIDDERIPPSVRLRLIERLAKAAGPEGMAVAGQADMEGEGKTLTLESELEYIH 180  
QY 175 KTKTGALLTFPAVMSAADIANVDYDTKEHLESYSLHGMFQIKDDLDCYGDDEAKLGKKV 234  
DB 181 RHKTKMLQYVHAQALIGADARQTRLEDFAAHLGLAFOIRDDIIDEGAEKIKGPV 240  
QY 235 GSDLENNKSTYVSLGKDGAEKLTYPHDAVDELTOID 273  
DB 241 GSDQSNKATYPALLSLAGAKKELAFHTEAQRHLRND 279

RESULT 8  
US-08-534-910B-8  
Sequence 8, Application US/08534910B  
Patent No. 5766911

GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOYAMA, Tanetsoshi  
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington

## STATE: DC

COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toftennet, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-8

Query Match 44.7%; Score 650; DB 1; Length 297;  
Best Local Similarity 47.3%; Pred. No. 1,36-56;  
Matches 132; Conservative 55; Mismatches 86; Indels 6; Gaps 2;

QY 1 MTNLPNKLIDEVNNELSVAINKSVM---DTOLEESMLYSLNAGGKRIPIVLLITLDS 56  
DB 1 MAQSVSEQFLNEQKQAVETALSRYIERLEGPAKVKKMAVSLKGGKRIPIVLLITLSTVQA 60  
QY 57 INTEVEYELGKSAIALEMHTYSLIHDDLPAVNDYRSGKLTNNKYGGWTAILAGDALL 116  
DB 61 LGKDPVAGLPVACALIEHTYSLIHDDLPSMNDLDRGKPTNNKYGGWTAILAGDALL 120  
QY 117 TKAFELIS--SDRLTDEVKIKVLRSLASGHVGMVGGQMLDMQSEGPIDLETLEMTH 174  
DB 121 TYAFQILTEIDDERIPPSVRLRLIERLAKAAGPEGMAVAGQADMEGEGKTLTLESELEYIH 180  
QY 175 KTKTGALLTFPAVMSAADIANVDYDTKEHLESYSLHGMFQIKDDLDCYGDDEAKLGKKV 234  
DB 181 RHKTKMLQYVHAQALIGADARQTRLEDFAAHLGLAFOIRDDIIDEGAEKIKGPV 240  
QY 235 GSDLENNKSTYVSLGKDGAEKLTYPHDAVDELTOID 273  
DB 241 GSDQSNKATYPALLSLAGAKKELAFHTEAQRHLRND 279

RESULT 9  
US-08-534-910B-10  
Sequence 10, Application US/08534910B  
Patent No. 5766911

GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOYAMA, Tanetsoshi  
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington

Tue Apr 20 12:43:41 2004

US-09-925-637-64\_1.rat

Page 5

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/ ADDRESSER: Kenyon & Kenyon
/ STREET: 1025 Connecticut Avenue, N.W., Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: U.S.
/ ZIP: 20036-5405
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.25" Floppy Disk
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
/ SOFTWARE: IBM/Word Perfect 6.1 Windows
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/534,910B
/ FILING DATE: 28-SEPT-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 7-25253
/ FILING DATE: 14-FEB-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Toifenetti, Judith L.
/ REGISTRATION NUMBER: 39,048
/ REFERENCE/DOCKET NUMBER: 77670/398
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)429-1776
/ TELEFAX: (202)429-0796
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 297 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Bacillus stearothermophilus
/
US-08-534-910B-10

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Query Match          44.7%; Score 650; DB 1; Length 297;
Best Local Similarity 47.3%; Pred. No. 1.3e-56;
Matches 132; Conservative 55; Mismatches 86; Indels 6; Gaps 2;

QY 1 MKNLIDVNNELSVAINKSVN---DTQLESMLYSINAGKRIIPVLLLTSLTIDS 56
DB 1 MAQLSEQPLNEQKQAVETALSRVIERLEGPAKKKAAVSLGAGKRIIPVLLTSTVOA 60
QY 57 LNTVEYELGKSAIALEMHTYSLIHDDLPAMNDVYRSGKLTNNHVVYGEWTAIIAGDALI 116
DB 61 LKQDPAVGIPIVACALIMHTYSLIHDDLPAMNDVYRSGKLTNNHVVYGEWTAIIAGDALI 120
QY 117 TYAFELIS--SDRLTDEVKIKVLORLSIASGHVGVGQMLDMQSEGPIDETLEMTH 174
DB 121 TYAFQILITIDDERIPPSVRLRIERLAKAAGPEGVAVGQAADMEGEGKTLTSLSELYIH 180
QY 175 KTRTGALLPFAVMSADIANDVDTTKEHLESYSHLGMVFOIKDILLCCYGEAKLGGKV 234
DB 181 RKHTGMLQYSVHAGLIGADARQREIDEPFAHLGLAFQIRDDILIDEGAEKIGKPV 240
QY 235 GSDLENNKSTYVSLGKGAEDKLTYYHRDAVDELTOID 273
DB 241 GSDQSNKATVPALLSLAGAKKELAFHIEAQRHLRNAD 279

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RESULT 10
US-09-367-528A-5
/ Sequence 5, Application US/09367528A
/ Patent No. 6395525
/ GENERAL INFORMATION:
/ APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
/ TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
/ FILE REFERENCE: PH-586
/ CURRENT APPLICATION NUMBER: US/09/367,528A
/ PRIOR FILING DATE: 1999-08-16
/ PRIOR APPLICATION NUMBER: JP97/346686
/ PRIOR FILING DATE: 1997-12-16
/ NUMBER OF SEQ ID NOS: 6

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/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 297
/ TYPE: PRT
/ ORGANISM: Bacillus stearothermophilus
/
US-09-367-528A-5

```

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Query Match          44.7%; Score 650; DB 4; Length 297;
Best Local Similarity 49.6%; Pred. No. 1.3e-56;
Matches 134; Conservative 49; Mismatches 85; Indels 2; Gaps 1;

QY 6 MKNLIDVNNELSVAINKSVMDTQLESMLYSINAGKRIIPVLLLTSLTIDSLNTEYELGM 65
DB 10 LNEQKQAVETALSRVIERLEGPAKKKAAVSLGAGKRIIPVLLTSTVRLGKDPVAVGL 69
QY 66 KSAIALEMHTYSLIHDDLPAMNDVYRSGKLTNNHVVYGEWTAIIAGDALITKAFELIS- 124
DB 70 PVACALIMHTYSLIHDDLPAMNDVYRSGKLTNNHVVYGEWTAIIAGDALITKAFELITE 129
QY 125 -SDRLTDEVKIKVLORLSIASGHVGVGQMLDMQSEGPIDETLEMTHKTGTGALLT 183
DB 130 IDDERIPPSVRLRIERLAKAAGPEGVAVGQAADMEGEGKTLTSLSELYIHRHKTGMLQ 189
QY 184 PAVMSADIANDVDTTKEHLESYSHLGMVFOIKDILLCCYGEAKLGGKVSQLENNKS 243
DB 190 YSVHAGLIGADARQREIDEPFAHLGLAFQIRDDILIDEGAEKIGKEVSGDSQNNKA 249
QY 244 TYVSLGKGAEDKLTYYHRDAVDELTOID 273
DB 250 TYPALLSLAGAKKELAFHIEAQRHLRNAD 279

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RESULT 11
US-09-367-528A-1
/ Sequence 1, Application US/09367528A
/ Patent No. 6395525
/ GENERAL INFORMATION:
/ APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
/ TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
/ FILE REFERENCE: PH-586
/ CURRENT APPLICATION NUMBER: US/09/367,528A
/ PRIOR FILING DATE: 1999-08-16
/ PRIOR APPLICATION NUMBER: JP97/346686
/ PRIOR FILING DATE: 1997-12-16
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 297
/ TYPE: PRT
/ ORGANISM: Bacillus stearothermophilus
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: 82
/ OTHER INFORMATION: Xaa represents Val, Leu, Ile, Thr, Asp, Glu, Asn, Gln, Lys,
/ OTHER INFORMATION: Arg, Cys, Met, Phe, Tyr, Trp, His or Pro.
/
US-09-367-528A-1

```

```

Query Match          44.5%; Score 646; DB 4; Length 297;
Best Local Similarity 49.3%; Pred. No. 3.3e-56;
Matches 133; Conservative 49; Mismatches 86; Indels 2; Gaps 1;

QY 6 MKNLIDVNNELSVAINKSVMDTQLESMLYSINAGKRIIPVLLLTSLTIDSLNTEYELGM 65
DB 10 LNEQKQAVETALSRVIERLEGPAKKKAAVSLGAGKRIIPVLLTSTVRLGKDPVAVGL 69
QY 66 KSAIALEMHTYSLIHDDLPAMNDVYRSGKLTNNHVVYGEWTAIIAGDALITKAFELIS- 124
DB 70 PVACALIMHTYSLIHDDLPAMNDVYRSGKLTNNHVVYGEWTAIIAGDALITKAFELITE 129
QY 125 -SDRLTDEVKIKVLORLSIASGHVGVGQMLDMQSEGPIDETLEMTHKTGTGALLT 183
DB 130 IDDERIPPSVRLRIERLAKAAGPEGVAVGQAADMEGEGKTLTSLSELYIHRHKTGMLQ 189

```

QY 184 FAVMSADIANDVDTTKEHLESYHLMGFQIKDDLLDCYGDENKLGKXGSDLENNKS 243  
 DB 190 YSVHAGALIGADANQRTREDEFAHGLAFQIRDDILIEGAEEKIGKPVSDOSNNKA 249  
 QY 244 TVVSLGKGADKLTYYRDAVDELTOID 273  
 DB 250 TVPALLSLAGAKKLAFFHIEAQRHLRND 279

RESULT 12  
 US-08-534-910B-6  
 / Sequence 6, Application US/08534910B  
 / Patent No. 5766911  
 / GENERAL INFORMATION:  
 / APPLICANT: KOIKE, Ayumi  
 / APPLICANT: OBATA, Shusei  
 / APPLICANT: NISHINO, Tokuzo  
 / APPLICANT: OHNUMA, Shinichi  
 / APPLICANT: NAKAZAWA, Takeshi  
 / APPLICANT: OGURA, Kyoze  
 / APPLICANT: Koyama, Taneosshi  
 / TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable  
 / TITLE OF INVENTION: Of Synthesizing Geranyl diphosphate And Gene Coding Ther  
 / NUMBER OF SEQUENCES: 10  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Kenyon & Kenyon  
 / STREET: 1025 Connecticut Avenue, N.W., Suite 600  
 / CITY: Washington  
 / STATE: DC  
 / COUNTRY: U.S.  
 / ZIP: 20036-5405  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: 3.25" Floppy Disk  
 / COMPUTER: IBM PC Compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
 / SOFTWARE: IBM/Word Perfect 6.1 Windows  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/534,910B  
 / FILING DATE: 28-SEPT-1995  
 / CLASSIFICATION: 435  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: JP 7-25253  
 / FILING DATE: 14-FEB-1995  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Toftennett, Judith L.  
 / REGISTRATION NUMBER: 39,048  
 / REFERENCE/DOCKET NUMBER: 77670/398  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (202)429-1776  
 / TELEFAX: (202)429-0796  
 / INFORMATION FOR SEQ ID NO: 6:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 297 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: protein  
 / ORIGINAL SOURCE:  
 / ORGANISM: Bacillus stearothermophilus  
 / US-08-534-910B-6

Query Match 44.4%; Score 645; DB 1; Length 297;  
 Best Local Similarity 48.0%; Pred. No. 4,2e-56;  
 Matches 130; Conservative 56; Mismatches 79; Indels 6; Gaps 2;

QY 1 MTNPMKLTDEVNNEISVAINKSVM-----DTQLEBSMTVSYNNGKRIRPVLLTLTDS 56  
 DB 1 MAQSVSEFNEKQAVETALSRYIERLEGPAKIKKMAVSLGGRIRPFLLSVRA 60  
 QY 57 INTEVELGKSAIILEMHTYSLIHDDLPAMDNDYRGRKLTNNKYGEWTAILAGDAL 116  
 DB 61 LGKPAVGLPVACALIEHHTSLIHDDLPAMDNDLRGRKPTNNKYVGEAMAILAGDGL 120  
 QY 117 TKAFELIS--SDDRITDEVKIKVLORISIASGHVGMGGOMLDMQSGQPIDETLEMIR 174

DB 121 TYAFQLTIDEIDEPISVRRLIERLAKAAGPBGVAGQADWEGKTLTSELVYIH 180  
 QY 175 KTKTGALITFAVMSADIANDVDTTKEHLESYHLMGFQIKDDLLDCYGDENKLGKXV 234  
 DB 181 RHKTGKMLQYSVHAGALIGADANQRTREDEFAHGLAFQIRDDILIEGAEEKIGKPV 240  
 QY 235 GSDLENNKSTVSVSLGKGADKLTYYRDA 265  
 DB 241 GSDOSNNKATTPALLSLAGAKKLAFFHIEA 271

RESULT 13  
 US-09-367-528A-3  
 / Sequence 3, Application US/09367528A  
 / Patent No. 6395525  
 / GENERAL INFORMATION:  
 / APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA  
 / TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene  
 / FILE REFERENCE: PH-586  
 / CURRENT APPLICATION NUMBER: US/09/367,528A  
 / PRIOR FILING DATE: 1999-08-16  
 / PRIOR APPLICATION NUMBER: JP97/346686  
 / NUMBER OF SEQ ID NOS: 6  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO 3  
 / LENGTH: 297  
 / TYPE: PRT  
 / ORGANISM: Bacillus stearothermophilus  
 / US-09-367-528A-3

Query Match 44.3%; Score 644; DB 4; Length 297;  
 Best Local Similarity 49.3%; Pred. No. 5.3e-56;  
 Matches 133; Conservative 49; Mismatches 86; Indels 2; Gaps 1;

QY 6 MNKLTDEVNNEISVAINKSVMDTQLEBSMTVSYNNGKRIRPVLLTLTDSINTEYELGM 65  
 DB 10 LNEQKQAVETALSRYIERLEGPAKIKKMAVSLGGRIRPFLLSVRAVLGKDPVGL 69  
 QY 66 KSAILEMHTYSLIHDDLPAMDNDYRGRKLTNNKYGEWTAILAGDALITKAFELIS- 124  
 DB 70 PVACALIEHHTYSLIHDDLPAMDNDLRGRKPTNNKYVGEAMAILAGDGLTYAFQLTITE 129  
 QY 125 -SDDRITDEVKIKVLORISIASGHVGMGGOMLDMQSGQPIDETLEMIRKTKGALLT 183  
 DB 130 IDDERIPSPVRRLIERLAKAAGPBGVAGQADWEGKTLTSELVYIRHKTGKMLQ 189  
 QY 184 FAVMSADIANDVDTTKEHLESYHLMGFQIKDDLLDCYGDENKLGKXGSDLENNKS 243  
 DB 190 YSVHAGALIGADANQRTREDEFAHGLAFQIRDDILIEGAEEKIGKPVSDOSNNKA 249  
 QY 244 TVVSLGKGADKLTYYRDAVDELTOID 273  
 DB 250 TVPALLSLAGAKKLAFFHIEAQRHLRND 279

RESULT 14  
 US-09-275-742-2  
 / Sequence 2, Application US/09275742  
 / Patent No. 6130069  
 / GENERAL INFORMATION:  
 / APPLICANT: Wilding, Edwin Imogen  
 / APPLICANT: Gwynn, Michael  
 / FILE REFERENCE: GM10205  
 / CURRENT APPLICATION NUMBER: US/09/275,742  
 / NUMBER OF SEQ ID NOS: 2  
 / SOFTWARE: FastSeq for Windows Version 3.0  
 / SEQ ID NO 2  
 / LENGTH: 291  
 / TYPE: PRT

ORGANISM: Streptococcus pneumoniae  
US-09-275-742-2

Query Match 37.9%; Score 551; DB 3; Length 291;  
Best Local Similarity 46.6%; Pred. No. 9.2e-47;  
Matches 122; Conservative 48; Mismatches 88; Indels 4; Gaps 3;

QY 28 TOLBSMYSINAGGKRIIPVLLITLDSLN-TELEMGKMAIAEMHTYSLIHDDIPA 86  
DB 25 SLSRSVLSIHAGGRRIRPFLIKVLELQVIRPAHQVATLAEMLHTSLIHDDIPA 84  
QY 87 MNDDYRRGKLTNKKYGEWTAIILAGDALITKAFELISSDRLTDEVKIKYQRLSIASG 146  
DB 85 MDDDDYRRGRLTNKKKFGEMALILAGDALFLDPYALIAQD-LPQGIKVGILANISLASG 143  
QY 147 HVGMVGGQMLDMQSEGPIDLETLEMIRKKTGALLTPAVMSADIIVNDTTKEHLESY 206  
DB 144 SIGMVAQVLDMEGEGHLSLEELQTIHANKTGKLLAYFQAAALIAELSPEMQVKLKTIV 203  
QY 207 SYHGMFQIKDLDLCYGDDEAKLGKVGSDLENNKSTYVSLIGKGAEDKLTTHRDAAV 266  
DB 204 GELIGLAFVDRDVLVTASFEIIGTKPQKDLQAEKSTIPALGLESTIAFCNQTLDQAN 263  
QY 267 DELTQIDEQ-FNTKHLIEIVD 286  
DB 264 DKLEBIAQQLPFETESIVSVE 285

# RESULT 15

US-09-107-532A-6724

Sequence 6724, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: CTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6724:

SEQUENCE CHARACTERISTICS:

LENGTH: 312 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

## FEATURE:

NAME/KEY: misc\_feature

LOCATION: (B) LOCATION 1...312

SEQUENCE DESCRIPTION: SEQ ID NO: 6724:

US-09-107-532A-6724

Query Match 36.7%; Score 533; DB 4; Length 312;  
Best Local Similarity 44.5%; Pred. No. 6.3e-45;  
Matches 117; Conservative 48; Mismatches 96; Indels 2; Gaps 2;

QY 13 VNNLSVAINKSVMDTOLBSMYSINAGGKRIIPVLLITLDSLNTEVELGM-KSAIAL 71  
DB 30 VEKELISFLDEHTTDRGLYDAMSYSVAGGKRIIPVLLITLAVASFEPIDVYQVAAL 89  
QY 72 EMHTYSLIHDDLPAMDNDYRRGKLTNKKYGEWTAIILAGDALITKAFELISSDRLTD 131  
DB 90 EMHTYSLIHDDLPAMDNDYRRGKLTNKKYGEWTAIILAGDALITKAFELISSDRLTD 148  
QY 132 EVKIKYVQLRLSIASGHVGMVGGQMLDMQSEGPIDLETLEMIRKKTGALLTPAVMSAD 191  
DB 149 SPFLILLQLAVAGAGGQVWAGQADIEGSKLSLEELAFIHERKTGHLIRYALLAGGI 208  
QY 192 IANVDTTKEHLESYSHLGMFQIKDLDLCYGDDEAKLGKVGSDLENNKSTYVSLIGK 251  
DB 209 LAKQPEBILHLQLRLHGLIAFQIRDDLDVIGTKTGKTAGKDERMEKNTYPRLLGL 268  
QY 252 DGAEDKLTTHRDAAVDELTOIDE 274  
DB 269 EKTREALEIELSANKIIDLEE 291

Search completed: April 19, 2004, 15:49:32  
Job time : 24 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 15:48:07 ; Search time 47 Seconds

(without alignments)  
1683.366 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 1453

Sequence: 1 MTNLLPMNKLIDEVNNELSLVA.....ELTQIDQENFKHLEIYDL 287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1124875 segs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubppa/US09C\_NEW\_PUB.pep.\*  
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15: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1453	100.0	287	9	US-09-925-637-64
2	1453	100.0	287	14	US-10-084-205-64
3	1444	99.4	293	12	US-10-282-122A-44363
4	1442	99.2	293	9	US-09-815-242-12583
5	1415	97.4	288	9	US-09-815-242-5239
6	1040	71.6	293	12	US-10-282-122A-71252
7	1015	69.9	293	12	US-10-282-122A-70715
8	702.5	48.3	293	12	US-10-282-122A-60940
9	650	44.7	297	12	US-10-462-698A-76
10	638	43.9	294	15	US-10-369-493-17358
11	636.5	43.8	272	15	US-10-369-493-23301
12	617	42.5	297	15	US-10-369-493-16549
13	615	42.3	296	12	US-10-282-122A-45490
14	596	41.0	293	9	US-09-815-242-10630
15	596	41.0	293	12	US-10-282-122A-57289

16	578.5	39.8	261	15	US-10-369-493-9710	Sequence 9710, Ap
17	568	39.1	295	12	US-10-282-122A-53246	Sequence 53246, A
18	557	38.3	294	12	US-10-282-122A-52706	Sequence 52706, A
19	556	38.3	290	15	US-10-369-493-20893	Sequence 20893, A
20	554	38.1	289	12	US-10-282-122A-72262	Sequence 72262, A
21	551.5	38.0	290	12	US-10-282-122A-74642	Sequence 74642, A
22	549	37.8	291	9	US-09-815-242-13597	Sequence 13597, A
23	547	37.6	291	9	US-09-815-242-13273	Sequence 13273, A
24	547	37.6	291	12	US-10-282-122A-73998	Sequence 73998, A
25	544.5	37.5	310	15	US-10-369-493-19922	Sequence 19922, A
26	541.5	37.3	265	12	US-10-282-122A-57443	Sequence 57443, A
27	540.5	37.2	285	15	US-10-369-493-18391	Sequence 18391, A
28	534.5	36.8	309	15	US-10-369-493-18752	Sequence 18752, A
29	532	36.6	289	12	US-10-282-122A-51526	Sequence 51526, A
30	526.5	36.2	302	15	US-10-369-493-2608	Sequence 2608, Ap
31	524	36.1	291	15	US-10-369-493-8506	Sequence 8506, Ap
32	516.5	35.5	297	9	US-09-934-903-14	Sequence 14, Appl
33	516.5	35.5	297	9	US-09-934-868-72	Sequence 72, Appl
34	516.5	35.5	297	10	US-09-941-947A-20	Sequence 20, Appl
35	516.5	35.5	297	12	US-10-700-003-14	Sequence 14, Appl
36	515.5	35.5	306	15	US-10-369-493-10187	Sequence 10187, A
37	504.5	34.7	367	13	US-10-108-915-26	Sequence 26, Appl
38	497.5	34.2	295	9	US-09-815-242-11239	Sequence 11239, A
39	497.5	34.2	295	12	US-10-282-122A-58515	Sequence 58515, A
40	495.5	34.1	296	15	US-10-369-493-21173	Sequence 21173, A
41	495.5	34.1	350	12	US-10-424-599-268482	Sequence 268482, A
42	494.5	34.1	353	12	US-10-425-114-47693	Sequence 47693, A
43	494.5	34.0	350	13	US-10-108-915-22	Sequence 22, Appl
44	492.5	33.9	268	12	US-10-282-122A-45768	Sequence 45768, A
45	492	33.9	287	15	US-10-369-493-19191	Sequence 19191, A

## ALIGNMENTS

RESULT 1  
US-09-925-637-64  
Sequence 64, Application US/09925637  
Patent No. US2002010338A1  
GENERAL INFORMATION:  
APPLICANT: Chai  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides  
FILE REFERENCE: P8560  
CURRENT APPLICATION NUMBER: US/09/925,637  
PRIOR APPLICATION NUMBER: PCT/US00/23773  
PRIOR FILING DATE: 2000-08-31  
PRIOR FILING DATE: 2000-08-31  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: US 08/781,986  
PRIOR FILING DATE: 1997-01-03  
PRIOR APPLICATION NUMBER: US 08/956,171  
PRIOR FILING DATE: 1997-10-20  
PRIOR APPLICATION NUMBER: US 60/009,861  
PRIOR FILING DATE: 1996-01-06  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 64  
LENGTH: 287  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-637-64  
Query Match 100.0%; Score 1453; DB 9; Length 287;  
Best Local Similarity 100.0%; Pred. No. 4.6e-139; Indels 0; Gaps 0;  
Matches 287; Conservative 0;  
1 MTNLLPMNKLIDEVNNELSLVA.....ELTQIDQENFKHLEIYDL 287  
1 MTNLLPMNKLIDEVNNELSLVA.....ELTQIDQENFKHLEIYDL 287  
61 YELGKSAIAEMHTYSLIHDDLPAMNDYRGGKLTNHYGVEMTAIAGDLITKAF 120

Db 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKVGEMTAIIAGDALLTKAF 120  
 QY 121 ELISSDRRLTDEVKIKYLOSLASIGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180  
 Db 121 ELISSDRRLTDEVKIKYLOSLASIGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180  
 QY 181 LITPAVMSAADIANVDPTTKEHLESYHIGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240  
 Db 181 LITPAVMSAADIANVDPTTKEHLESYHIGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240  
 QY 241 NKSTYVSLGKDGAEKLTYYHRDAVDELTOIDEQFNTKHLLEIVDL 287  
 Db 241 NKSTYVSLGKDGAEKLTYYHRDAVDELTOIDEQFNTKHLLEIVDL 287

## RESULT 2

US-10-084-205-64  
 ; Sequence 64, Application US/10084205  
 ; Publication No. US20030049648A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Choi, Gil  
 ; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides  
 ; FILE REFERENCE: P815P1  
 ; CURRENT APPLICATION NUMBER: US/10/084,205  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23773  
 ; PRIOR FILING DATE: 2000-08-31  
 ; PRIOR APPLICATION NUMBER: 60/151,933  
 ; PRIOR FILING DATE: 1999-09-01  
 ; NUMBER OF SEQ ID NOS: 74  
 ; SOFTWARE: PatentIn Ver. 3.1  
 ; SEQ ID NO 64  
 ; LENGTH: 287  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus aureus  
 US-10-084-205-64

Query Match 100.0%; Score 1453; DB 14; Length 287;  
 Best Local Similarity 100.0%; Pred. No. 4,6e-139;  
 Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTNLPNKLIDEVNNELSVAINKSYMDTOLESMLYSINAGKRIKRPVLLITLDSINTE 60  
 Db 1 MTNLPNKLIDEVNNELSVAINKSYMDTOLESMLYSINAGKRIKRPVLLITLDSINTE 60  
 QY 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKVGEMTAIIAGDALLTKAF 120  
 Db 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKVGEMTAIIAGDALLTKAF 120  
 QY 121 ELISSDRRLTDEVKIKYLOSLASIGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180  
 Db 121 ELISSDRRLTDEVKIKYLOSLASIGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180  
 QY 181 LITPAVMSAADIANVDPTTKEHLESYHIGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240  
 Db 181 LITPAVMSAADIANVDPTTKEHLESYHIGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240  
 QY 241 NKSTYVSLGKDGAEKLTYYHRDAVDELTOIDEQFNTKHLLEIVDL 287  
 Db 241 NKSTYVSLGKDGAEKLTYYHRDAVDELTOIDEQFNTKHLLEIVDL 287

## RESULT 3

US-10-282-122A-44363  
 ; Sequence 44363, Application US/10282122A  
 ; Publication No. US20040029129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Kari  
 ; APPLICANT: Zykkind, Judith

; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Foreyth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 ; FILE REFERENCE: ELITRA.034A  
 ; CURRENT APPLICATION NUMBER: US/10/282,122A  
 ; PRIOR FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See file Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 78614  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 44363  
 ; LENGTH: 293  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus aureus  
 US-10-282-122A-44363

Query Match 99.4%; Score 1444; DB 12; Length 293;  
 Best Local Similarity 99.3%; Pred. No. 3.9e-138;  
 Matches 285; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTNLPNKLIDEVNNELSVAINKSYMDTOLESMLYSINAGKRIKRPVLLITLDSINTE 60  
 Db 1 MTNLPNKLIDEVNNELSVAINKSYMDTOLESMLYSINAGKRIKRPVLLITLDSINTE 60  
 QY 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKVGEMTAIIAGDALLTKAF 120  
 Db 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKVGEMTAIIAGDALLTKAF 120  
 QY 121 ELISSDRRLTDEVKIKYLOSLASIGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180  
 Db 121 ELISSDRRLTDEVKIKYLOSLASIGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180  
 QY 181 LITPAVMSAADIANVDPTTKEHLESYHIGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240  
 Db 181 LITPAVMSAADIANVDPTTKEHLESYHIGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240  
 QY 241 NKSTYVSLGKDGAEKLTYYHRDAVDELTOIDEQFNTKHLLEIVDL 287  
 Db 241 NKSTYVSLGKDGAEKLTYYHRDAVDELTOIDEQFNTKHLLEIVDL 287

## RESULT 4

US-09-815-242-12583  
 ; Sequence 12583, Application US/09815242  
 ; Patent No. US20020061569A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Kari L.  
 ; APPLICANT: Zykkind, Judith W.  
 ; APPLICANT: Wall, Daniel

```

; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12583
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12583

Query Match          99.3%; Score 1442; DB 9; Length 293;
Best Local Similarity 99.3%; Pred. No. 6,2e-138;
Matches 285; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 MTNLPNNKLIDEVNNELSAVINKSVMDTQLESMLYSINAGGKRIRPVLLLTLSLNTFELGM 60
QY 61 YELGMSALALEMITHYSLIHDDLPMNDNDYRGGKLTNKKYGEWTAIIAGDALLTKAF 120
DB 61 YELGMSALALEMITHYSLIHDDLPMNDNDYRGGKLTNKKYGEWTAIIAGDALLTKAF 120
QY 121 ELISSDRLTDEYKIKVQLRLSIASGHVGVGQMLDMSGQPIDLETLEMIMHKTGTGA 180
DB 121 ELISSDRLTDEYKIKVQLRLSIASGHVGVGQMLDMSGQPIDLETLEMIMHKTGTGA 180
QY 181 LITFAVMSAADIANVDDTKHEHLESYSYHLGMMFOIKDILLDCYGEAKLGKVGSDLEN 240
DB 181 LITFAVMSAADIANVDDTKHEHLESYSYHLGMMFOIKDILLDCYGEAKLGKVGSDLEN 240
QY 241 NKSTVYSLGKGAEDKLTYHRDAVDELTOIDEGENTHLEIYDL 287
DB 241 NKSTVYSLGKGAEDKLTYHRDAVDELTOIDEGENTHLEIYDL 287

RESULT 5
US-09-815-242-5239
; Sequence 5239, Application US/09815242
; Patent No. US20020061569X1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
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; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5239
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5239

Query Match          97.4%; Score 1415; DB 9; Length 288;
Best Local Similarity 99.3%; Pred. No. 3.4e-135;
Matches 280; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 MKKLIDEVNNELSAVINKSVMDTQLESMLYSINAGGKRIRPVLLLTLSLNTFELGM 65
DB 1 MKKLIDEVNNELSAVINKSVMDTQLESMLYSINAGGKRIRPVLLLTLSLNTFELGM 60
QY 66 KSAIHALEMITHYSLIHDDLPMNDNDYRGGKLTNKKYGEWTAIIAGDALLTKAFELISS 125
DB 61 KSAIHALEMITHYSLIHDDLPMNDNDYRGGKLTNKKYGEWTAIIAGDALLTKAFELISS 120
QY 126 DDLRLTDEYKIKVQLRLSIASGHVGVGQMLDMSGQPIDLETLEMIMHKTGTALLTFA 185
DB 121 DDLRLTDEYKIKVQLRLSIASGHVGVGQMLDMSGQPIDLETLEMIMHKTGTALLTFA 180
QY 186 VMSAADIANVDDTKHEHLESYSYHLGMMFOIKDILLDCYGEAKLGKVGSDLENNKSTY 245
DB 181 VMSAADIANVDDTKHEHLESYSYHLGMMFOIKDILLDCYGEAKLGKVGSDLENNKSTY 240
QY 246 VSLGKGAEDKLTYHRDAVDELTOIDEGENTHLEIYDL 287
DB 241 VSLGKGAEDKLTYHRDAVDELTOIDEGENTHLEIYDL 282

RESULT 6
US-10-282-122A-71252
; Sequence 71252, Application US/10282122A
; Publication No. US20040029129X1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
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/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO: 71252
/ LENGTH: 293
/ TYPE: PRF
/ ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-71252
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Query Match 71.6%; Score 1040; DB 12; Length 293;
Best Local Similarity 69.0%; Pred. No. 4.5e-97;
Matches 198; Conservative 42; Mismatches 47; Indels 0; Gaps 0;
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QY 1 MTNLPMNKLIDVNNELSVAINKSVMDQLEBSMLYSNAGGKRIRPVLLITLDSLNT 60
DB 1 MAKSMANLINOINSALGCVETSPINTNLESQYSLNAGGKRIRPVLLITLDSLNT 60
QY 61 YELGKSAIALEMIHITSLIHDDLPAMNDYRRGKLTNNKVGEMWTAIIAGDALLTKAF 120
DB 61 YKKGKTLALEMIHITSLIHDDLPAMNDYRRGKLTNNKVGEMWTAIIAGDALLTKAF 120
QY 121 ELISDDRLTDEVKIKVLQRLSIASGHVGMVGOMLMOSEGPDLFTLEMIHKTGTA 180
DB 121 ELIADDELLESVKKILSRILANSGLMGVGGQLDMQSEDKVDLTLEFQIHAKTGA 180
QY 181 LITPAVMSADIANVDITKEHLESYHLCGMFQIKDLDLCYGEAKLGKVGSDLEN 240
DB 181 LITPAVMSADIANVDITKEHLESYHLCGMFQIKDLDLCYGEAKLGKVGSDLEN 240
QY 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
DB 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
QY 241 HKSTYVSLIGKGAEDKLTFRDAVDELTOIDQFNTKHLLEIVDL 287
DB 241 HKSTYVSLIGKGAEDKLTFRDAVDELTOIDQFNTKHLLEIVDL 287
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RESULT 7
US-10-282-122A-70715
/ Sequence 70715, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyckind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282.122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
```

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/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO: 70715
/ LENGTH: 293
/ TYPE: PRF
/ ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70715
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Query Match 69.9%; Score 1015; DB 12; Length 293;
Best Local Similarity 68.6%; Pred. No. 1.6e-94;
Matches 197; Conservative 41; Mismatches 49; Indels 0; Gaps 0;
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QY 1 MTNLPMNKLIDVNNELSVAINKSVMDQLEBSMLYSNAGGKRIRPVLLITLDSLNT 60
DB 1 MKKQMNKLININSLNSIOSPLKTRLEBSMKYSNAGGKRIRPVLLITLDSLNT 60
QY 61 YELGKSAIALEMIHITSLIHDDLPAMNDYRRGKLTNNKVGEMWTAIIAGDALLTKAF 120
DB 61 YQGGNSALALAMIHITSLIHDDLPAMNDYRRGKLTNNKVGEMWTAIIAGDALLTKAF 120
QY 121 ELISDDRLTDEVKIKVLQRLSIASGHVGMVGOMLMOSEGPDLFTLEMIHKTGTA 180
DB 121 ELISDDRLTDEVKIKVLQRLSIASGHVGMVGOMLMOSEGPDLFTLEMIHKTGTA 180
QY 181 LITPAVMSADIANVDITKEHLESYHLCGMFQIKDLDLCYGEAKLGKVGSDLEN 240
DB 181 LITPAVMSADIANVDITKEHLESYHLCGMFQIKDLDLCYGEAKLGKVGSDLEN 240
QY 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
DB 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
QY 241 HKSTYVSLIGKGAEDKLTFRDAVDELTOIDQFNTKHLLEIVDL 287
DB 241 HKSTYVSLIGKGAEDKLTFRDAVDELTOIDQFNTKHLLEIVDL 287
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RESULT 8
US-10-282-122A-60940
/ Sequence 60940, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyckind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282.122A
/ CURRENT FILING DATE: 2003-02-20
```







TYPE: PRT  
ORGANISM: Bacillus anthracis  
US-10-282-122A-45490

Query Match 42.3%; Score 615; DB 12; Length 296;  
Best Local Similarity 46.2%; Pred. No. 7, 1e-54;  
Matches 128; Conservative 56; Mismatches 89; Indels 4; Gaps 2;

QY 13 VNNEISVAINKSVMDTOLEESMTLSINAGKRIRPVLLTLDLNTNEYELGMSALALE 72  
DB 16 VEEKIVASANEQCNVIREANVSLGSKRRLPLFATLOAFDERNLGVGAACALE 75  
QY 73 MIHTYSLIHDDLPMANDDYRGKLTNNKYVGWTAIAGDALLTKAFELISS--DDRLT 130  
DB 76 MIHTYSLVHDDLPCMDDDDLRGRKPTNNKVFGEAMAVIAGDGLLTVAFOVIMAYGQKEIS 135  
QY 131 DEVKIKVLOKSLASGHVGMVGQMLDMQSGQPIDLETLEMINKTKTGALLTFAVMSAA 190  
DB 136 AEKRVLYLEAKAGPBGWVGQVADAEAGKOLTTIDLEYIKHKTKGLLEPAVLAGS 195  
QY 191 DIANVDTTKEHLESYSYHLGMMFOIKDILLDCYGDCAKLGKXGSDLENKSKTYVSILG 250  
DB 196 ILSDBTEQGEKLEFPAKYGAFQIRDDIDVETSEIEIKRPGSDVSNKSTYTTLLFT 255  
QY 251 KDGAEKLTTHRDAAVDELTOIDEGFNTKHLLEIVDL 287  
DB 256 VDRADILDETAKAKDAIGSL--QLQDEYLLSICDL 290

RESULT 14  
US-09-815-242-10630

Sequence 10630, Application US/09815242  
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Wall, Daniel

APPLICANT: Zykkind, Judith W.

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10630

LENGTH: 293

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-815-242-10630

Query Match 41.0%; Score 596; DB 9; Length 293;  
Best Local Similarity 46.0%; Pred. No. 5, 9e-52;  
Matches 134; Conservative 56; Mismatches 91; Indels 10; Gaps 5;

QY 1 MTNLPMN--KLIDEVNNEISVAINKSVMDTOLEESMTLSINAGKRIRPVLLTLDLSIN 58  
DB 1 MTNFSQCHLPLVEKRWVDF---IAETNERLEKENTLVIHGGKRLRLVLVTTAAAG 57  
QY 59 TEYEL-GMSAIALEMIHTYSLIHDDLPMANDDYRGKLTNNKYVGWTAIAGDALLT 117  
DB 58 KEMETODYVVAASLEMIHTYSLIHDDLPMADDLDRGRPTNNKVFGEATVAILAGDGLT 117  
QY 118 KAPELSSDDRLTDEVKIKVLOKSLASGHVGMVGQMLDMQSGQPIDLETLEMINKTK 177  
DB 118 GAFQSLSLSQLGISE-KVLMQQLAKAGNQGVMGDIEGKYSLTLESLAAVHEKK 176  
QY 178 TGAULTFAVMSAADIANVDTTKEHLESYSYHLGMMFOIKDILLDCYGDCAKLGKXGSD 237  
DB 177 TGALEFALVAGVLANQTEEVYGLLTQFAHHYGLAFQIRDDLLDATSTEADLGKXGRD 236  
QY 238 LENKSTYVSILGKGAEDKLT--HRDAVDELTOIDEGFNTKHLLEIV 285  
DB 237 EALNKSTYPALGIGAGAKDALTQLAEGSAVLEKTAVPNPSSEHLANLL 287

RESULT 15  
US-10-282-122A-57289

Sequence 57289, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl

APPLICANT: Zykkind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 57289

LENGTH: 293

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-10-282-122A-57289

Query Match 41.0%; Score 596; DB 12; Length 293;  
Best Local Similarity 46.0%; Pred. No. 5, 9e-52;

